

part
A

Tue Jul 17 14:16:55 2001 [BLASTN 2.1.3 [Apr-1-2001], NCBI]
/home/ruby/va/Molbio/carpenda/temp1/ss.DNA40981 (2906 bp)

Sequences producing High-scoring Segment Pairs:					Frame	Score	Match	Pct	E-val
1	P_AAC97475	Human angiogenesis-associated protein PR	+	2906	2906	100	0.0		
2	P_AAF44261	Human PRO331 nucleotide sequence SEQ ID	+	2906	2906	100	0.0		
3	P_AAF72423	Human PRO331 cDNA.	+	2906	2906	100	0.0		
4	P_AAZ52207	Human PRO331 protein encoding cDNA, UNQ2	+	2906	2906	100	0.0		
5	P_AAA77596	Human PRO331 cDNA sequence SEQ ID NO:106	+	2906	2906	100	0.0		
6	P_AAX52265	Protein PRO331 cDNA clone DNA40981-1234.	+	2906	2906	100	0.0		
7	AX098385	Sequence 11 from Patent WO0119991.	+	2906	2906	100	0.0		
8	AB046800	Homo sapiens mRNA for KIAA1580 protein,	+	2889	2898	100	0.0		
9	AC021820	Homo sapiens clone RP11-40H19, WORKING D	+	2136	2136	100	0.0		
10	AC080100	Homo sapiens chromosome 11 clone RP11-45	-	2132	2135	100	0.0		

>1 P_AAC97475 Human angiogenesis-associated protein PRO331 cDNA, SEQ ID NO:136.
(2906 bp) [1 seg]
Score = 2906 (5761 bits), Expect = 0.0
Identities = 2906/2906 (100%), at 1,1-2906,2906, Strand +/-

BLAST RESULTS A-1

DNA40981	1	GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGG
P_AAC97475	1	GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGG
DNA40981	61	TGCCTTGCAAAAATGAAGGATGCAGGACGCAGCTTTCCTCGGAACCGAACGCAATGGAT
P_AAC97475	61	TGCCTTGCAAAAATGAAGGATGCAGGACGCAGCTTTCCTCGGAACCGAACGCAATGGAT
DNA40981	121	AAACTGATTGTGCAAGAGAGAAGGAAGAACGAAGCTTTTTCTTGTGAGCCCTGGATCTTA
P_AAC97475	121	AAACTGATTGTGCAAGAGAGAAGGAAGAACGAAGCTTTTTCTTGTGAGCCCTGGATCTTA
DNA40981	181	ACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAATAAACAGAGTTAGA
P_AAC97475	181	ACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAATAAACAGAGTTAGA
DNA40981	241	CCCGCGGGGGTTGGTGTGTCTGACATAAATAAATAATCTTAAAGCAGCTGTTCCCTCC
P_AAC97475	241	CCCGCGGGGGTTGGTGTGTCTGACATAAATAAATAATCTTAAAGCAGCTGTTCCCTCC
DNA40981	301	CCACCCCCAAAAAAGGATGATTGGAAATGAAGAACCGAGGATTCACAAAGAAAAAAGT
P_AAC97475	301	CCACCCCCAAAAAAGGATGATTGGAAATGAAGAACCGAGGATTCACAAAGAAAAAAGT
DNA40981	361	ATGTTTCATTTTTCTCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTTTGGAATGAAAAG
P_AAC97475	361	ATGTTTCATTTTTCTCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTTTGGAATGAAAAG
DNA40981	421	TTTGGGGCTTTTTTAGTAAAGTAAAGAACTGGTGTGGTGGTGTTCCTTTCTTTTGGAA
P_AAC97475	421	TTTGGGGCTTTTTTAGTAAAGTAAAGAACTGGTGTGGTGGTGTTCCTTTCTTTTGGAA
DNA40981	481	TTTCCCACAAGAGGAGAGGAAATTAATAATACATCTGCAAAGAAATTTTCAGAGAAGAAAA
P_AAC97475	481	TTTCCCACAAGAGGAGAGGAAATTAATAATACATCTGCAAAGAAATTTTCAGAGAAGAAAA
DNA40981	541	GTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACCAGCAGAGCACAGTTGGA
P_AAC97475	541	GTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACCAGCAGAGCACAGTTGGA
DNA40981	601	TTTGTGCCTATGTTGACTAAAATTGACGGATAATTGCAGTTGGATTTTTCTTCATCAACC

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P_AAC97475 601 TTTGTGCCTATGTTGACTAAAATTGACGGATAATTGCAGTTGGATTTTCTTCATCAACC
DNA40981 661 TCCTTTTTTTTAAATTTTTATTCCTTTTGGTATCAAGATCATGCGTTTTCTCTTGTTCTT
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P_AAC97475 661 TCCTTTTTTTTAAATTTTTATTCCTTTTGGTATCAAGATCATGCGTTTTCTCTTGTTCTT
DNA40981 721 AACCACCTGGATTTCCATCTGGATGTTGCTGTGATCAGTCTGAAATACAACCTGTTTGAAT
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P_AAC97475 721 AACCACCTGGATTTCCATCTGGATGTTGCTGTGATCAGTCTGAAATACAACCTGTTTGAAT
DNA40981 781 TCCAGAAGGACCAACACCAGATAAATTATGAATGTTGAACAAGATGACCTTACATCCACA
*****
P_AAC97475 781 TCCAGAAGGACCAACACCAGATAAATTATGAATGTTGAACAAGATGACCTTACATCCACA
DNA40981 841 GCAGATAATGATAGGTCCTAGGTTTAAACAGGGCCCTATTTGACCCCCTGCTTGTGGTGCT
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P_AAC97475 841 GCAGATAATGATAGGTCCTAGGTTTAAACAGGGCCCTATTTGACCCCCTGCTTGTGGTGCT
DNA40981 901 GCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGCGGGCTCAGACCTGCCCTTCTGT
*****
P_AAC97475 901 GCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGCGGGCTCAGACCTGCCCTTCTGT
DNA40981 961 GTGCTCCTGCAGCAACCAGTTCAGCAAGGTGATTTGTGTTCGGAAAAACCTGCGTGAGGT
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P_AAC97475 961 GTGCTCCTGCAGCAACCAGTTCAGCAAGGTGATTTGTGTTCGGAAAAACCTGCGTGAGGT
DNA40981 1021 TCCGGATGGCATCTCCACCAACACACGGCTGCTGAACCTCCATGAGAACCAAATCCAGAT
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P_AAC97475 1021 TCCGGATGGCATCTCCACCAACACACGGCTGCTGAACCTCCATGAGAACCAAATCCAGAT
DNA40981 1081 CATCAAAGTGAACAGCTTCAAGCACTTGAGGCACTTGGAATCCTACAGTTGAGTAGGAA
*****
P_AAC97475 1081 CATCAAAGTGAACAGCTTCAAGCACTTGAGGCACTTGGAATCCTACAGTTGAGTAGGAA
DNA40981 1141 CCATATCAGAACCATTGAAATTGGGGCTTTCAATGGTCTGGCGAACCTCAACACTCTGGA
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P_AAC97475 1141 CCATATCAGAACCATTGAAATTGGGGCTTTCAATGGTCTGGCGAACCTCAACACTCTGGA
DNA40981 1201 ACTCTTTGACAATCGTCTTACTACCATCCCGAATGGAGCTTTTGTATACCTGTCTAAACT
*****
P_AAC97475 1201 ACTCTTTGACAATCGTCTTACTACCATCCCGAATGGAGCTTTTGTATACCTGTCTAAACT
DNA40981 1261 GAAGGAGCTCTGGTTGCGAAACAACCCCATTTGAAAGCATCCCTTCTTATGCTTTTAAACAG
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P_AAC97475 1261 GAAGGAGCTCTGGTTGCGAAACAACCCCATTTGAAAGCATCCCTTCTTATGCTTTTAAACAG
DNA40981 1321 AATTCCTTCTTTGCGCCGACTAGACTTAGGGGAATTGAAAAGACTTTCATACATCTCAGA
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P_AAC97475 1321 AATTCCTTCTTTGCGCCGACTAGACTTAGGGGAATTGAAAAGACTTTCATACATCTCAGA
DNA40981 1381 AGGTGCCTTTGAAGGTCTGTCCAACCTTGAGGTATTTGAACCTTGCCATGTGCAACCTTCG
*****
P_AAC97475 1381 AGGTGCCTTTGAAGGTCTGTCCAACCTTGAGGTATTTGAACCTTGCCATGTGCAACCTTCG
DNA40981 1441 GGAAATCCCTAACCTCACACCGCTCATAAACTAGATGAGCTGGATCTTTCTGGGAATCA
*****
P_AAC97475 1441 GGAAATCCCTAACCTCACACCGCTCATAAACTAGATGAGCTGGATCTTTCTGGGAATCA
DNA40981 1501 TTTATCTGCCATCAGGCCTGGCTCTTTCCAGGGTTTGATGCACCTTCAAAAACCTGTGGAT
*****
P_AAC97475 1501 TTTATCTGCCATCAGGCCTGGCTCTTTCCAGGGTTTGATGCACCTTCAAAAACCTGTGGAT
DNA40981 1561 GATACAGTCCCAGATTCAAGTGATTGAACGGAATGCCCTTTGACAACCTTCAGTCACTAGT

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BLAST RESULTS A-2

BLAST RESULTS A-3.

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P_AAC97475 1561 GATACAGTCCCAGATTCAAGTGATTGAACGGAATGCCTTTGACAACCTTCAGTCACTAGT
DNA40981 1621 GGAGATCAACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTTCACTCCCTT
*****
P_AAC97475 1621 GGAGATCAACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTTCACTCCCTT
DNA40981 1681 GCATCATCTAGAGCGGATACATTTACATCACAACCCTTGGAAGTGTAACTGTGACATACT
*****
P_AAC97475 1681 GCATCATCTAGAGCGGATACATTTACATCACAACCCTTGGAAGTGTAACTGTGACATACT
DNA40981 1741 GTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTTGTGCCCGGTG
*****
P_AAC97475 1741 GTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTTGTGCCCGGTG
DNA40981 1801 TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCAC
*****
P_AAC97475 1801 TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCAC
DNA40981 1861 ATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACCTGAAGGCATGGC
*****
P_AAC97475 1861 ATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACCTGAAGGCATGGC
DNA40981 1921 AGCTGAGCTGAAATGTCGGGCCCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAA
*****
P_AAC97475 1921 AGCTGAGCTGAAATGTCGGGCCCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAA
DNA40981 1981 TGGAACAGTCATGACACATGGGGCGTACAAAGTGC GGATAGCTGTGCTCAGTGATGGTAC
*****
P_AAC97475 1981 TGGAACAGTCATGACACATGGGGCGTACAAAGTGC GGATAGCTGTGCTCAGTGATGGTAC
DNA40981 2041 GTTAAATTTACAAAATGTAACGTGCAAGATACAGGCATGTACACATGTATGGTGAGTAA
*****
P_AAC97475 2041 GTTAAATTTACAAAATGTAACGTGCAAGATACAGGCATGTACACATGTATGGTGAGTAA
DNA40981 2101 TTCCGTTGGGAATACTACTGCTTCAGCCACCCTGAATGTTACTGCAGCAACCCTACTCC
*****
P_AAC97475 2101 TTCCGTTGGGAATACTACTGCTTCAGCCACCCTGAATGTTACTGCAGCAACCCTACTCC
DNA40981 2161 TTTCTCTTACTTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG
*****
P_AAC97475 2161 TTTCTCTTACTTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG
DNA40981 2221 GACCACAGATAACAATGTGGGTCCCACTCCAGTGGTTCGACTGGGAGACCACCAATGTGAC
*****
P_AAC97475 2221 GACCACAGATAACAATGTGGGTCCCACTCCAGTGGTTCGACTGGGAGACCACCAATGTGAC
DNA40981 2281 CACCTCTCTCACACCACAGAGCACAAGGTCGACAGAGAAAACCTTCACCATCCCAGTGAC
*****
P_AAC97475 2281 CACCTCTCTCACACCACAGAGCACAAGGTCGACAGAGAAAACCTTCACCATCCCAGTGAC
DNA40981 2341 TGATATAAACAGTGGGATCCCAGGAATTGATGAGGTCATGAAGACTACCAAAATCATCAT
*****
P_AAC97475 2341 TGATATAAACAGTGGGATCCCAGGAATTGATGAGGTCATGAAGACTACCAAAATCATCAT
DNA40981 2401 TGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCATTTTCTACAAGAT
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DNA40981 2461 GAGGAAGCAGCACCATCGGCAAAACCATCACGCCCCAACAAGGACTGTTGAAATTATTAA
*****
P_AAC97475 2461 GAGGAAGCAGCACCATCGGCAAAACCATCACGCCCCAACAAGGACTGTTGAAATTATTAA
DNA40981 2521 TGTGGATGATGAGATTACGGGAGACACACCCATGGAAAGCCACCTGCCCATGCCTGCTAT
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P_AAC97475 2521 TGTGGATGATGAGATTACGGGAGACACACCCATGGAAAGCCACCTGCCCATGCCTGCTAT
DNA40981 2581 CGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTTCAACCACACAACAAC
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P_AAC97475 2581 CGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTTCAACCACACAACAAC
DNA40981 2641 AGTTAACACAATAAATTCAATACACAGTTCAGTGCATGAACCGTTATTGATCCGAATGAA
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P_AAC97475 2641 AGTTAACACAATAAATTCAATACACAGTTCAGTGCATGAACCGTTATTGATCCGAATGAA
DNA40981 2701 CTCTAAAGACAATGTACAAGAGACTCAAATCTAAAACATTTACAGAGTTACAAAAAACAA
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DNA40981 2761 ACAATCAAAAAAAGACAGTTTATTAATAATGACACAAATGACTGGGCTAAATCTACTG
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P_AAC97475 2761 ACAATCAAAAAAAGACAGTTTATTAATAATGACACAAATGACTGGGCTAAATCTACTG
DNA40981 2821 TTTCAAAAAAGTGTCTTTACAAAAAACAAAAAGAAAAGAAATTTATTTATTAATAAT
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P_AAC97475 2821 TTTCAAAAAAGTGTCTTTACAAAAAACAAAAAGAAAAGAAATTTATTTATTAATAAT
DNA40981 2881 CTATTGTGATCTAAAGCAGACAAAAA
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P_AAC97475 2881 CTATTGTGATCTAAAGCAGACAAAAA

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>2 P_AAF44261 Human PRO331 nucleotide sequence SEQ ID NO:500. (2906 bp) [1 seg]
Score = 2906 (5761 bits), Expect = 0.0
Identities = 2906/2906 (100%), at 1,1-2906,2906, Strand +/-

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DNA40981 1 GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGG
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P_AAF44261 1 GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGG
DNA40981 61 TGCCTTGCAAAAATGAAGGATGCAGGACGCAGCTTTCCTCGGAACCGAACGCAATGGAT
*****
P_AAF44261 61 TGCCTTGCAAAAATGAAGGATGCAGGACGCAGCTTTCCTCGGAACCGAACGCAATGGAT
DNA40981 121 AAACGTGATTGTGCAAGAGAGAAGGAAGAACGAAGCTTTTTCTTGTGAGCCCTGGATCTTA
*****
P_AAF44261 121 AAACGTGATTGTGCAAGAGAGAAGGAAGAACGAAGCTTTTTCTTGTGAGCCCTGGATCTTA
DNA40981 181 ACACAAATGTGTATATGTGCACACAGGGAGCATTCAGAATGAAATAAACAGAGTTAGA
*****
P_AAF44261 181 ACACAAATGTGTATATGTGCACACAGGGAGCATTCAGAATGAAATAAACAGAGTTAGA
DNA40981 241 CCCGCGGGGGTTGGTGTGTTCTGACATAAAATAAATAATCTTAAAGCAGCTGTTCCCCCTCC
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P_AAF44261 241 CCCGCGGGGGTTGGTGTGTTCTGACATAAAATAAATAATCTTAAAGCAGCTGTTCCCCCTCC
DNA40981 301 CCACCCCCAAAAAAGGATGATTGGAATGAAGAACCGAGGATTCACAAAGAAAAAAGT
*****
P_AAF44261 301 CCACCCCCAAAAAAGGATGATTGGAATGAAGAACCGAGGATTCACAAAGAAAAAAGT
DNA40981 361 ATGTTCAATTTTTCTCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTTTGGAATGAAAAG
*****
P_AAF44261 361 ATGTTCAATTTTTCTCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTTTGGAATGAAAAG
DNA40981 421 TTTGGGGCTTTTTTAGTAAAGTAAAGAACTGGTGTGGTGGTGTTCCTTTCTTTTTGAA
*****
P_AAF44261 421 TTTGGGGCTTTTTTAGTAAAGTAAAGAACTGGTGTGGTGGTGTTCCTTTCTTTTTGAA
DNA40981 481 TTTCCCAAGAGGAGAGGAAATTAATAATACATCTGCAAGAAATTTACAGAGAAGAAAA

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BLAST RESULTS A-4

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P_AAF44261 481 TTTCCCACAAGAGGAGAGGAAATTAATAATACATCTGCAAAGAAATTTTCAGAGAAGAAAA
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P_AAF44261 541 GTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACCAGCAGAGCACAGTTGGA
DNA40981 601 TTTGTGCCTATGTTGACTAAAATTGACGGATAATTGCAGTTGGATTTTCTTCATCAACC
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P_AAF44261 601 TTTGTGCCTATGTTGACTAAAATTGACGGATAATTGCAGTTGGATTTTCTTCATCAACC
DNA40981 661 TCCTTTTTTTTAAATTTTTTATTCTTTTGGTATCAAGATCATGCGTTTTCTCTTGTTCTT
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P_AAF44261 661 TCCTTTTTTTTAAATTTTTTATTCTTTTGGTATCAAGATCATGCGTTTTCTCTTGTTCTT
DNA40981 721 AACCACCTGGATTTCCATCTGGATGTTGCTGTGATCAGTCTGAAATACAACCTGTTTGAAT
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P_AAF44261 721 AACCACCTGGATTTCCATCTGGATGTTGCTGTGATCAGTCTGAAATACAACCTGTTTGAAT
DNA40981 781 TCCAGAAGGACCAACACCAGATAAATTATGAATGTTGAACAAGATGACCTTACATCCACA
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P_AAF44261 781 TCCAGAAGGACCAACACCAGATAAATTATGAATGTTGAACAAGATGACCTTACATCCACA
DNA40981 841 GCAGATAATGATAGGTCCTAGGTTTAACAGGGCCCTATTTGACCCCTGCTTGTGGTGCT
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P_AAF44261 841 GCAGATAATGATAGGTCCTAGGTTTAACAGGGCCCTATTTGACCCCTGCTTGTGGTGCT
DNA40981 901 GCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGC GGCTCAGACCTGCCCTTCTGT
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P_AAF44261 901 GCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGC GGCTCAGACCTGCCCTTCTGT
DNA40981 961 GTGCTCCTGCAGCAACCAGTTCAGCAAGGTGATTTGTGTTCGGAAAAACCTGCGTGAGGT
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P_AAF44261 961 GTGCTCCTGCAGCAACCAGTTCAGCAAGGTGATTTGTGTTCGGAAAAACCTGCGTGAGGT
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DNA40981 1081 CATCAAAGTGAACAGCTTCAAGCACTTGAGGCATTGGAAATCCTACAGTTGAGTAGGAA
*****
P_AAF44261 1081 CATCAAAGTGAACAGCTTCAAGCACTTGAGGCATTGGAAATCCTACAGTTGAGTAGGAA
DNA40981 1141 CCATATCAGAACCATTGAAATTGGGGCTTTCAATGGTCTGGCGAACCTCAACACTCTGGA
*****
P_AAF44261 1141 CCATATCAGAACCATTGAAATTGGGGCTTTCAATGGTCTGGCGAACCTCAACACTCTGGA
DNA40981 1201 ACTCTTTGACAATCGTCTTACTACCATCCCGAATGGAGCTTTTGTATACTTGTCTAAACT
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P_AAF44261 1201 ACTCTTTGACAATCGTCTTACTACCATCCCGAATGGAGCTTTTGTATACTTGTCTAAACT
DNA40981 1261 GAAGGAGCTCTGGTTGCGAAACAACCCCATTGAAAGCATCCCTTCTTATGCTTTTAACAG
*****
P_AAF44261 1261 GAAGGAGCTCTGGTTGCGAAACAACCCCATTGAAAGCATCCCTTCTTATGCTTTTAACAG
DNA40981 1321 AATTCCTTCTTTGCGCCGACTAGACTTAGGGGAATTGAAAAGACTTTTCATACATCTCAGA
*****
P_AAF44261 1321 AATTCCTTCTTTGCGCCGACTAGACTTAGGGGAATTGAAAAGACTTTTCATACATCTCAGA
DNA40981 1381 AGGTGCCTTTGAAGGTCTGTCCAACCTTGAGGTATTTGAACCTTGCCATGTGCAACCTTCG
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P_AAF44261 1381 AGGTGCCTTTGAAGGTCTGTCCAACCTTGAGGTATTTGAACCTTGCCATGTGCAACCTTCG
DNA40981 1441 GGAAATCCCTAACCTCACACCGCTCATAAAACCTAGATGAGCTGGATCTTTCTGGGAATCA

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BLAST RESULTS A-5

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P_AAF44261 1441 GGAAATCCCTAACCTCACACCGCTCATAAACTAGATGAGCTGGATCTTTCTGGGAATCA
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P_AAF44261 1501 TTTATCTGCCATCAGGCCTGGCTCTTTCCAGGGTTTGATGCACCTTCAAAAACGTGGAT
DNA40981 1561 GATACAGTCCCAGATTCAAGTGATTGAACGGAATGCCTTTGACAACCTTCAGTCACTAGT
*****
P_AAF44261 1561 GATACAGTCCCAGATTCAAGTGATTGAACGGAATGCCTTTGACAACCTTCAGTCACTAGT
DNA40981 1621 GGAGATCAACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTTCACTCCCTT
*****
P_AAF44261 1621 GGAGATCAACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTTCACTCCCTT
DNA40981 1681 GCATCATCTAGAGCGGATACATTTACATCACAACCCTTGGAACGTGAACGTGTGACATACT
*****
P_AAF44261 1681 GCATCATCTAGAGCGGATACATTTACATCACAACCCTTGGAACGTGAACGTGTGACATACT
DNA40981 1741 GTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTGTGCCCCGGTG
*****
P_AAF44261 1741 GTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTGTGCCCCGGTG
DNA40981 1801 TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCAC
*****
P_AAF44261 1801 TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCAC
DNA40981 1861 ATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGC
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P_AAF44261 1861 ATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGC
DNA40981 1921 AGCTGAGCTGAAATGTCGGGCCCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAA
*****
P_AAF44261 1921 AGCTGAGCTGAAATGTCGGGCCCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAA
DNA40981 1981 TGGAACAGTCATGACACATGGGGCGTACAAAGTGC GGATAGCTGTGCTCAGTGATGGTAC
*****
P_AAF44261 1981 TGGAACAGTCATGACACATGGGGCGTACAAAGTGC GGATAGCTGTGCTCAGTGATGGTAC
DNA40981 2041 GTTAAATTTACAAAATGTAACGTGTGCAAGATACAGGCATGTACACATGTATGGTGAGTAA
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P_AAF44261 2041 GTTAAATTTACAAAATGTAACGTGTGCAAGATACAGGCATGTACACATGTATGGTGAGTAA
DNA40981 2101 TTCCGTTGGGAATACTACTGCTTCAGCCACCCTGAATGTTACTGCAGCAACCACTACTCC
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P_AAF44261 2101 TTCCGTTGGGAATACTACTGCTTCAGCCACCCTGAATGTTACTGCAGCAACCACTACTCC
DNA40981 2161 TTTCTCTTACTTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG
*****
P_AAF44261 2161 TTTCTCTTACTTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG
DNA40981 2221 GACCACAGATAACAATGTGGGTCCCACTCCAGTGGTCTGACTGGGAGACCACCAATGTGAC
*****
P_AAF44261 2221 GACCACAGATAACAATGTGGGTCCCACTCCAGTGGTCTGACTGGGAGACCACCAATGTGAC
DNA40981 2281 CACCTCTCTCACACCACAGAGCACAAGGTCGACAGAGAAAACCTTCACCATCCCAGTGAC
*****
P_AAF44261 2281 CACCTCTCTCACACCACAGAGCACAAGGTCGACAGAGAAAACCTTCACCATCCCAGTGAC
DNA40981 2341 TGATATAAACAGTGGGATCCCAGGAATTGATGAGGTCATGAAGACTACCAAAATCATCAT
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P_AAF44261 2341 TGATATAAACAGTGGGATCCCAGGAATTGATGAGGTCATGAAGACTACCAAAATCATCAT
DNA40981 2401 TGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCAATTTCTACAAGAT

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BLAST RESULTS A-6

P_AAF44261 2401 TGGGTGTTTGTGGCCATCACACTCATGGCTGCAGTGA

DNA40981 2461 GAGGAAGCAGCACCATCGGCAAAACCATCACGCCCCAACATTTCTACAAGAT

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DNA40981 2581 CGAGCATGAGCACCTAAATCACTATAACTCATACAATCTCCCTTCAACCACAT

P_AAF44261 2581 CGAGCATGAGCACCTAAATCACTATAACTCATACAATCTCCCTTCAACCACAT

DNA40981 2641 AGTTAACACAATAAATTCATACAGTTCAGTGCATGAACCGTTATTGATCCGAATGA

P_AAF44261 2641 AGTTAACACAATAAATTCATACAGTTCAGTGCATGAACCGTTATTGATCCGAATGA

DNA40981 2701 CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTTACAGAGTTACAAAAACAA

P_AAF44261 2701 CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTTACAGAGTTACAAAAACAA

DNA40981 2761 ACAATCAAAAAAAGACAGTTTATTAATAATGACACAAATGACTGGGCTAAATCTACTG

P_AAF44261 2761 ACAATCAAAAAAAGACAGTTTATTAATAATGACACAAATGACTGGGCTAAATCTACTG

DNA40981 2821 TTTCAAAAAAGTGTCTTTACAAAAAACAAAAAGAAATTTATTTATTAATAAT

P_AAF44261 2821 TTTCAAAAAAGTGTCTTTACAAAAAACAAAAAGAAATTTATTTATTAATAAT

DNA40981 2881 CTATTGTGATCTAAAGCAGACAAAA

P_AAF44261 2881 CTATTGTGATCTAAAGCAGACAAAA

>3 P_AAF72423 Human PRO331 cDNA. (2906 bp) [1 seg]
Score = 2906 (5761 bits), Expect = 0.0
Identities = 2906/2906 (100%), at 1,1-2906,2906, Strand +/-

DNA40981 1 GGGGAGAGGAATTGACCATGTAAAGGAGACTTTTTTTTGGTGGTGGTGGTGGTGGTGGG

P_AAF72423 1 GGGGAGAGGAATTGACCATGTAAAGGAGACTTTTTTTTGGTGGTGGTGGTGGTGGTGGG

DNA40981 61 TGCCTTGCAAAAATGAAGGATGCAGGACGAGCTTTCTCCTGGAACCGAATGGAT

P_AAF72423 61 TGCCTTGCAAAAATGAAGGATGCAGGACGAGCTTTCTCCTGGAACCGAATGGAT

DNA40981 121 AAATGATTTGTGCAAGAGAGAAGGAACGAAGCTTTTCTTGTGAGCCCTGGATCTTA

P_AAF72423 121 AAATGATTTGTGCAAGAGAGAAGGAACGAAGCTTTTCTTGTGAGCCCTGGATCTTA

DNA40981 181 ACACAAATGTGTATATGTGCACACAGGAGCATTCAGAATGAAATAAACCAGAGTTAGA

P_AAF72423 181 ACACAAATGTGTATATGTGCACACAGGAGCATTCAGAATGAAATAAACCAGAGTTAGA

DNA40981 241 CCCGCGGGGTTGGTGTGTTCTGACATAAATAAATCTTAAAGCAGCTGTCCCCCTCC

P_AAF72423 241 CCCGCGGGGTTGGTGTGTTCTGACATAAATAAATCTTAAAGCAGCTGTCCCCCTCC

DNA40981 301 CCACCCCAAAAAAAGGATGATTGGAATGAAGACCGAGGATTACAAAGAAAAAGT

P_AAF72423 301 CCACCCCAAAAAAAGGATGATTGGAATGAAGACCGAGGATTACAAAGAAAAAGT

DNA40981 361 ATGTTCAATTTTCTCTATAAAGGAGAAAGTGAGCAAGGAGATATTTTGAATGAAAG

BLAST RESULTS A-F

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*****
P_AAF72423 361 ATGTTTCATTTTTCTCTATAAAGGAGAAAGT̃GAGCCAAGGAGATATTTTTGGAATGAAAAG
DNA40981 421 TTTGGGGCTTTTTTAGTAAAGTAAAGAACTGGTGTGGTGGTGTTCCTTTCTTTTTGAA
*****
P_AAF72423 421 TTTGGGGCTTTTTTAGTAAAGTAAAGAACTGGTGTGGTGGTGTTCCTTTCTTTTTGAA
DNA40981 481 TTTCCCACAAGAGGAGAGGAAATTAATAATACATCTGCAAAGAAATTCAGAGAAGAAAA
*****
P_AAF72423 481 TTTCCCACAAGAGGAGAGGAAATTAATAATACATCTGCAAAGAAATTCAGAGAAGAAAA
DNA40981 541 GTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACCAGCAGAGCACAGTTGGA
*****
P_AAF72423 541 GTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACCAGCAGAGCACAGTTGGA
DNA40981 601 TTTGTGCCATATGTTGACTAAAATTGACGGATAATTGCAGTTGGATTTTTCTTCATCAACC
*****
P_AAF72423 601 TTTGTGCCATATGTTGACTAAAATTGACGGATAATTGCAGTTGGATTTTTCTTCATCAACC
DNA40981 661 TCCTTTTTTTTTAAATTTTTATTCCTTTTGGTATCAAGATCATGCGTTTTCTCTTGTTCTT
*****
P_AAF72423 661 TCCTTTTTTTTTAAATTTTTATTCCTTTTGGTATCAAGATCATGCGTTTTCTCTTGTTCTT
DNA40981 721 AACCACCTGGATTTCCATCTGGATGTTGCTGTGATCAGTCTGAAATACAACGTGTTGAAT
*****
P_AAF72423 721 AACCACCTGGATTTCCATCTGGATGTTGCTGTGATCAGTCTGAAATACAACGTGTTGAAT
DNA40981 781 TCCAGAAGGACCAACACCAGATAAATTATGAATGTTGAACAAGATGACCTTACATCCACA
*****
P_AAF72423 781 TCCAGAAGGACCAACACCAGATAAATTATGAATGTTGAACAAGATGACCTTACATCCACA
DNA40981 841 GCAGATAATGATAGGTCCTAGGTTTAACAGGGCCCTATTTGACCCCTGCTTGTGGTGCT
*****
P_AAF72423 841 GCAGATAATGATAGGTCCTAGGTTTAACAGGGCCCTATTTGACCCCTGCTTGTGGTGCT
DNA40981 901 GCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGCGGGCTCAGACCTGCCCTTCTGT
*****
P_AAF72423 901 GCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGCGGGCTCAGACCTGCCCTTCTGT
DNA40981 961 GTGCTCCTGCAGCAACCAGTTCAGCAAGGTGATTTGTGTTGCGAAAAACCTGCGTGAGGT
*****
P_AAF72423 961 GTGCTCCTGCAGCAACCAGTTCAGCAAGGTGATTTGTGTTGCGAAAAACCTGCGTGAGGT
DNA40981 1021 TCCGGATGGCATCTCCACCAACACACGGCTGCTGAACCTCCATGAGAACCAAATCCAGAT
*****
P_AAF72423 1021 TCCGGATGGCATCTCCACCAACACACGGCTGCTGAACCTCCATGAGAACCAAATCCAGAT
DNA40981 1081 CATCAAAGTGAACAGCTTCAAGCACTTGAGGCATTGGAAATCCTACAGTTGAGTAGGAA
*****
P_AAF72423 1081 CATCAAAGTGAACAGCTTCAAGCACTTGAGGCATTGGAAATCCTACAGTTGAGTAGGAA
DNA40981 1141 CCATATCAGAACCATTGAAATTGGGGCTTTCAATGGTCTGGCGAACCTCAACACTCTGGA
*****
P_AAF72423 1141 CCATATCAGAACCATTGAAATTGGGGCTTTCAATGGTCTGGCGAACCTCAACACTCTGGA
DNA40981 1201 ACTCTTTGACAATCGTCTTACTACCATCCCGAATGGAGCTTTTGTATACTTGTCTAAACT
*****
P_AAF72423 1201 ACTCTTTGACAATCGTCTTACTACCATCCCGAATGGAGCTTTTGTATACTTGTCTAAACT
DNA40981 1261 GAAGGAGCTCTGGTTGCGAAACAACCCCATTTGAAAGCATCCCTTCTTATGCTTTTAACAG
*****
P_AAF72423 1261 GAAGGAGCTCTGGTTGCGAAACAACCCCATTTGAAAGCATCCCTTCTTATGCTTTTAACAG
DNA40981 1321 AATTCCTTCTTTGCGCCGACTAGACTTAGGGGAATTGAAAAGACTTTCATACATCTCAGA

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BLAST RESULTS A-8

P_AAF72423 1321 AATTCCTTCTTTGCGCCGACTAGACTTAGGGG.
DNA40981 1381 AGGTGCCTTTGAAGGTCTGTCCAACCTTGAGGTATT

P_AAF72423 1381 AGGTGCCTTTGAAGGTCTGTCCAACCTTGAGGTATTTGAAGACATCTCAGA
DNA40981 1441 GGAAATCCCTAACCTCACACCGCTCATAAACTAGATGAGCTGGACCTTCG

P_AAF72423 1441 GGAAATCCCTAACCTCACACCGCTCATAAACTAGATGAGCTGGATCTCTTCG
DNA40981 1501 TTTATCTGCCATCAGGCCTGGCTCTTTCCAGGGTTTGATGCACCTTCAAAATCA

P_AAF72423 1501 TTTATCTGCCATCAGGCCTGGCTCTTTCCAGGGTTTGATGCACCTTCAAAACTG
DNA40981 1561 GATACAGTCCCAGATTCAAGTGATTGAACGGAATGCCTTTGACAACCTTCAGTCACTAGT

P_AAF72423 1561 GATACAGTCCCAGATTCAAGTGATTGAACGGAATGCCTTTGACAACCTTCAGTCACTAGT
DNA40981 1621 GGAGATCAACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTTCACTCCCTT

P_AAF72423 1621 GGAGATCAACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTTCACTCCCTT
DNA40981 1681 GCATCATCTAGAGCGGATACATTTACATCACAACCCTTGGAAGTGTGACATACT

P_AAF72423 1681 GCATCATCTAGAGCGGATACATTTACATCACAACCCTTGGAAGTGTGACATACT
DNA40981 1741 GTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTGTGCCCCGGTG

P_AAF72423 1741 GTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTGTGCCCCGGTG
DNA40981 1801 TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCAC

P_AAF72423 1801 TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCAC
DNA40981 1861 ATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGC

P_AAF72423 1861 ATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGC
DNA40981 1921 AGCTGAGCTGAAATGTCGGGCCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAA

P_AAF72423 1921 AGCTGAGCTGAAATGTCGGGCCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAA
DNA40981 1981 TGGAACAGTCATGACACATGGGGCGTACAAAGTGCAGGATAGCTGTGCTCAGTGATGGTAC

P_AAF72423 1981 TGGAACAGTCATGACACATGGGGCGTACAAAGTGCAGGATAGCTGTGCTCAGTGATGGTAC
DNA40981 2041 GTTAAATTTACAAATGTAAGTGTGCAAGATACAGGCATGTACACATGTATGGTGAGTAA

P_AAF72423 2041 GTTAAATTTACAAATGTAAGTGTGCAAGATACAGGCATGTACACATGTATGGTGAGTAA
DNA40981 2101 TTCCGTTGGGAATACTACTGCTTCAGCCACCCTGAATGTTACTGCAGCAACCACTACTCC

P_AAF72423 2101 TTCCGTTGGGAATACTACTGCTTCAGCCACCCTGAATGTTACTGCAGCAACCACTACTCC
DNA40981 2161 TTTCTCTTACTTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG

P_AAF72423 2161 TTTCTCTTACTTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG
DNA40981 2221 GACCACAGATAACAATGTGGGTCCCAGTCCAGTGGTTCGACTGGGAGACCACCAATGTGAC

P_AAF72423 2221 GACCACAGATAACAATGTGGGTCCCAGTCCAGTGGTTCGACTGGGAGACCACCAATGTGAC
DNA40981 2281 CACCTCTCTCACACCACAGAGACAAGGTCGACAGAGAAAACCTTCACCATCCCAGTGAC

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P_AAF72423 2281 CACCTCTCTCACACCACAGAGCACAAGGTC
DNA40981 2341 TGATATAAACAGTGGGATCCCAGGAATTGATGAGG
P_AAF72423 2341 TGATATAAACAGTGGGATCCCAGGAATTGATGAGGTCAT
DNA40981 2401 TGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGATCATCAT
P_AAF72423 2401 TGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCAATCAT
DNA40981 2461 GAGGAAGCAGCACCATCGGCAAAACCATCACGCCCAACAAGGACTGTTGAAAT
P_AAF72423 2461 GAGGAAGCAGCACCATCGGCAAAACCATCACGCCCAACAAGGACTGTTGAAATTA
DNA40981 2521 TGTGGATGATGAGATTACGGGAGACACACCCATGGAAGCCACCTGCCCATGCCTGCTAT
P_AAF72423 2521 TGTGGATGATGAGATTACGGGAGACACACCCATGGAAGCCACCTGCCCATGCCTGCTAT
DNA40981 2581 CGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTTCAACCACACAACAAC
P_AAF72423 2581 CGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTTCAACCACACAACAAC
DNA40981 2641 AGTTAACACAATAAATTCAATACACAGTTCAGTGCATGAACCGTTATTGATCCGAATGAA
P_AAF72423 2641 AGTTAACACAATAAATTCAATACACAGTTCAGTGCATGAACCGTTATTGATCCGAATGAA
DNA40981 2701 CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTTACAGAGTTACAAAAACAA
P_AAF72423 2701 CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTTACAGAGTTACAAAAACAA
DNA40981 2761 ACAATCAAAAAAAGACAGTTTATTAATAATGACACAAATGACTGGGCTAAATCTACTG
P_AAF72423 2761 ACAATCAAAAAAAGACAGTTTATTAATAATGACACAAATGACTGGGCTAAATCTACTG
DNA40981 2821 TTTCAAAAAAGTGCTTTTACAAAAAACAAAAAGAAATTTATTTATTAATAAT
P_AAF72423 2821 TTTCAAAAAAGTGCTTTTACAAAAAACAAAAAGAAATTTATTTATTAATAAT
DNA40981 2881 CTATTGTGATCTAAAGCAGACAAAAA
P_AAF72423 2881 CTATTGTGATCTAAAGCAGACAAAAA

>4 P_AAZ52207 Human PRO331 protein encoding cDNA, UNQ292. DNA, PAT 18-JUL-2000
(2906 bp) [1 seg]
Score = 2906 (5761 bits), Expect = 0.0
Identities = 2906/2906 (100%), at 1,1-2906,2906, Strand +/-

DNA40981 1 GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGG
P_AAZ52207 1 GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGG
DNA40981 61 TGCCTTGCAAAAATGAAGGATGCAGGACGCAGCTTTCTCCTGGAACCGAACGCAATGGAT
P_AAZ52207 61 TGCCTTGCAAAAATGAAGGATGCAGGACGCAGCTTTCTCCTGGAACCGAACGCAATGGAT
DNA40981 121 AAAGTATTGTGCAAGAGAGAAGGAAGAACGAAGCTTTTTCTTGTGAGCCCTGGATCTTA
P_AAZ52207 121 AAAGTATTGTGCAAGAGAGAAGGAAGAACGAAGCTTTTTCTTGTGAGCCCTGGATCTTA
DNA40981 181 ACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAATAAACAGAGTTAGA
P_AAZ52207 181 ACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAATAAACAGAGTTAGA

10-A-10
10-A-10
10-A-10

DNA40981 241 CCCGCGGGGGTTGGTGTGTTCTGACATAAATAAA

P_AAZ52207 241 CCCGCGGGGGTTGGTGTGTTCTGACATAAATAAAT

DNA40981 301 CCACCCCCAAAAAAGGATGATTGGAAATGAAGAACCGAGGTTCCCCTCC

P_AAZ52207 301 CCACCCCCAAAAAAGGATGATTGGAAATGAAGAACCGAGGATT

DNA40981 361 ATGTTTCATTTTTCTCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTT

P_AAZ52207 361 ATGTTTCATTTTTCTCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTT

DNA40981 421 TTTGGGGCTTTTTTAGTAAAGTAAAGAACTGGTGTGGTGGTGTTCCTTTCTTT

P_AAZ52207 421 TTTGGGGCTTTTTTAGTAAAGTAAAGAACTGGTGTGGTGGTGTTCCTTTCTTT

DNA40981 481 TTTCCCACAAGAGGAGAGGAAATTAATAATACATCTGCAAAGAAATTCAGAGAAGAAAA

P_AAZ52207 481 TTTCCCACAAGAGGAGAGGAAATTAATAATACATCTGCAAAGAAATTCAGAGAAGAAAA

DNA40981 541 GTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACCAGCAGACAGTTGGA

P_AAZ52207 541 GTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACCAGCAGACAGTTGGA

DNA40981 601 TTTGTGCCTATGTTGACTAAAATTGACGGATAATTGCAGTTGGATTTTTCTTCATCAACC

P_AAZ52207 601 TTTGTGCCTATGTTGACTAAAATTGACGGATAATTGCAGTTGGATTTTTCTTCATCAACC

DNA40981 661 TCCTTTTTTTTAAATTTTTATTCCTTTTGGTATCAAGATCATGCGTTTTCTCTTGTCTTT

P_AAZ52207 661 TCCTTTTTTTTAAATTTTTATTCCTTTTGGTATCAAGATCATGCGTTTTCTCTTGTCTTT

DNA40981 721 AACCACCTGGATTTCATCTGGATGTTGCTGTGATCAGTCTGAAATACAACCTGTTTGAAT

P_AAZ52207 721 AACCACCTGGATTTCATCTGGATGTTGCTGTGATCAGTCTGAAATACAACCTGTTTGAAT

DNA40981 781 TCCAGAAGGACCAACACCAGATAAATTATGAATGTTGAACAAGATGACCTTACATCCACA

P_AAZ52207 781 TCCAGAAGGACCAACACCAGATAAATTATGAATGTTGAACAAGATGACCTTACATCCACA

DNA40981 841 GCAGATAATGATAGGTCCTAGGTTTAAACAGGGCCCTATTGACCCCCTGCTTGTGGTGCT

P_AAZ52207 841 GCAGATAATGATAGGTCCTAGGTTTAAACAGGGCCCTATTGACCCCCTGCTTGTGGTGCT

DNA40981 901 GCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGCGGGCTCAGACCTGCCCTTCTGT

P_AAZ52207 901 GCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGCGGGCTCAGACCTGCCCTTCTGT

DNA40981 961 GTGCTCCTGCAGCAACCAGTTCAGCAAGGTGATTGTGTTTCGGAAAAACCTGCGTGAGGT

P_AAZ52207 961 GTGCTCCTGCAGCAACCAGTTCAGCAAGGTGATTGTGTTTCGGAAAAACCTGCGTGAGGT

DNA40981 1021 TCCGGATGGCATCTCCACCAACACACGGCTGCTGAACCTCCATGAGAACCAATCCAGAT

P_AAZ52207 1021 TCCGGATGGCATCTCCACCAACACACGGCTGCTGAACCTCCATGAGAACCAATCCAGAT

DNA40981 1081 CATCAAAGTGAACAGCTTCAAGCACTTGAGGCATTGGAAATCCTACAGTTGAGTAGGAA

P_AAZ52207 1081 CATCAAAGTGAACAGCTTCAAGCACTTGAGGCATTGGAAATCCTACAGTTGAGTAGGAA

DNA40981 1141 CCATATCAGAACCATTGAAATTGGGGCTTTCAATGGTCTGGCGAACCTCAACACTCTGGA

P_AAZ52207 1141 CCATATCAGAACCATTGAAATTGGGGCTTTCAATGGTCTGGCGAACCTCAACACTCTGGA

RESULTS A-11

DNA40981	1201	ACTCTTTGACAATCGTCTTACTACCATCCCGAATGGAGCTTTTGTATACTTGTCTAAACT
P_AAZ52207	1201	ACTCTTTGACAATCGTCTTACTACCATCCCGAATGGAGCTTTTGTATACTTGTCTAAACT
DNA40981	1261	GAAGGAGCTCTGGTTGCGAAACAACCCCATTTGAAAGCATCCCTTCTTATGCTTTTAACAG
P_AAZ52207	1261	GAAGGAGCTCTGGTTGCGAAACAACCCCATTTGAAAGCATCCCTTCTTATGCTTTTAACAG
DNA40981	1321	AATTCCTTCTTTGCGCCGACTAGACTTAGGGGAATTGAAAAGACTTTCATACATCTCAGA
P_AAZ52207	1321	AATTCCTTCTTTGCGCCGACTAGACTTAGGGGAATTGAAAAGACTTTCATACATCTCAGA
DNA40981	1381	AGGTGCCTTTGAAGGTCTGTCCAACCTTGAGGTATTTGAACCTTGCCATGTGCAACCTTCG
P_AAZ52207	1381	AGGTGCCTTTGAAGGTCTGTCCAACCTTGAGGTATTTGAACCTTGCCATGTGCAACCTTCG
DNA40981	1441	GGAAATCCCTAACCTCACACCGCTCATAAACTAGATGAGCTGGATCTTTCTGGGAATCA
P_AAZ52207	1441	GGAAATCCCTAACCTCACACCGCTCATAAACTAGATGAGCTGGATCTTTCTGGGAATCA
DNA40981	1501	TTTATCTGCCATCAGGCCTGGCTCTTTCCAGGGTTTGATGCACCTTCAAAAACGTGGAT
P_AAZ52207	1501	TTTATCTGCCATCAGGCCTGGCTCTTTCCAGGGTTTGATGCACCTTCAAAAACGTGGAT
DNA40981	1561	GATACAGTCCCAGATTCAAGTGATTGAACGGAATGCCTTTGACAACCTTCAGTCACTAGT
P_AAZ52207	1561	GATACAGTCCCAGATTCAAGTGATTGAACGGAATGCCTTTGACAACCTTCAGTCACTAGT
DNA40981	1621	GGAGATCAACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTTCACCTCCCTT
P_AAZ52207	1621	GGAGATCAACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTTCACCTCCCTT
DNA40981	1681	GCATCATCTAGAGCGGATACATTTACATCACAACCCCTTGGAACGTAACTGTGACATACT
P_AAZ52207	1681	GCATCATCTAGAGCGGATACATTTACATCACAACCCCTTGGAACGTAACTGTGACATACT
DNA40981	1741	GTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTGTGCCCGGTG
P_AAZ52207	1741	GTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTGTGCCCGGTG
DNA40981	1801	TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCAC
P_AAZ52207	1801	TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCAC
DNA40981	1861	ATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGC
P_AAZ52207	1861	ATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGC
DNA40981	1921	AGCTGAGCTGAAATGTCGGGCCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAA
P_AAZ52207	1921	AGCTGAGCTGAAATGTCGGGCCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAA
DNA40981	1981	TGGAACAGTCATGACACATGGGGCGTACAAAAGTGC GGATAGCTGTGCTCAGTGATGGTAC
P_AAZ52207	1981	TGGAACAGTCATGACACATGGGGCGTACAAAAGTGC GGATAGCTGTGCTCAGTGATGGTAC
DNA40981	2041	GTTAAATTTACAAAATGTAAGTGTGCAAGATACAGGCATGTACACATGTATGGTGAGTAA
P_AAZ52207	2041	GTTAAATTTACAAAATGTAAGTGTGCAAGATACAGGCATGTACACATGTATGGTGAGTAA
DNA40981	2101	TTCCGTTGGGAATACTACTGCTTCAGCCACCCTGAATGTTACTGCAGCAACCACTACTCC
P_AAZ52207	2101	TTCCGTTGGGAATACTACTGCTTCAGCCACCCTGAATGTTACTGCAGCAACCACTACTCC

BLAST RESULTS A-12

DNA40981 2161 TTTCTCTTACTTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG

P_AAZ52207 2161 TTTCTCTTACTTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG

DNA40981 2221 GACCACAGATAACAATGTGGGTCCCACTCCAGTGGTCGACTGGGAGACCACCAATGTGAC

P_AAZ52207 2221 GACCACAGATAACAATGTGGGTCCCACTCCAGTGGTCGACTGGGAGACCACCAATGTGAC

DNA40981 2281 CACCTCTCTCACACCACAGAGCACAAGGTCGACAGAGAAAACCTTCACCATCCCAGTGAC

P_AAZ52207 2281 CACCTCTCTCACACCACAGAGCACAAGGTCGACAGAGAAAACCTTCACCATCCCAGTGAC

DNA40981 2341 TGATATAAACAGTGGGATCCCAGGAATTGATGAGGTCATGAAGACTACCAAAATCATCAT

P_AAZ52207 2341 TGATATAAACAGTGGGATCCCAGGAATTGATGAGGTCATGAAGACTACCAAAATCATCAT

DNA40981 2401 TGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCATTTTCTACAAGAT

P_AAZ52207 2401 TGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCATTTTCTACAAGAT

DNA40981 2461 GAGGAAGCAGCACCATCGGCAAAACCATCACGCCCCAACCAAGGACTGTTGAAATTATTAA

P_AAZ52207 2461 GAGGAAGCAGCACCATCGGCAAAACCATCACGCCCCAACCAAGGACTGTTGAAATTATTAA

DNA40981 2521 TGTGGATGATGAGATTACGGGAGACACACCCATGGAAAGCCACCTGCCCATGCCTGCTAT

P_AAZ52207 2521 TGTGGATGATGAGATTACGGGAGACACACCCATGGAAAGCCACCTGCCCATGCCTGCTAT

DNA40981 2581 CGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTTCAACCACACAACAAC

P_AAZ52207 2581 CGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTTCAACCACACAACAAC

DNA40981 2641 AGTTAACACAATAAATTCAATACACAGTTCAGTGCATGAACCGTTATTGATCCGAATGAA

P_AAZ52207 2641 AGTTAACACAATAAATTCAATACACAGTTCAGTGCATGAACCGTTATTGATCCGAATGAA

DNA40981 2701 CTCTAAAGACAATGTACAAGAGACTCAAATCTAAAACATTTACAGAGTTACAAAAACAA

P_AAZ52207 2701 CTCTAAAGACAATGTACAAGAGACTCAAATCTAAAACATTTACAGAGTTACAAAAACAA

DNA40981 2761 ACAATCAAAAAAAGACAGTTTATTAAAAATGACACAAATGACTGGGCTAAATCTACTG

P_AAZ52207 2761 ACAATCAAAAAAAGACAGTTTATTAAAAATGACACAAATGACTGGGCTAAATCTACTG

DNA40981 2821 TTTCAAAAAGTGTCTTTACAAAAAACAAAAAGAAAAGAAATTTATTTATTAATAAT

P_AAZ52207 2821 TTTCAAAAAGTGTCTTTACAAAAAACAAAAAGAAAAGAAATTTATTTATTAATAAT

DNA40981 2881 CTATTGTGATCTAAAGCAGACAAAAA

P_AAZ52207 2881 CTATTGTGATCTAAAGCAGACAAAAA

>5 P_AAA77596 Human PRO331 cDNA sequence SEQ ID NO:106. DNA, PAT 07-NOV-2000
(2906 bp) [1 seg]
Score = 2906 (5761 bits), Expect = 0.0
Identities = 2906/2906 (100%), at 1,1-2906,2906, Strand +/-

DNA40981 1 GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTTGGTGGTGGTGGCTGTTGGG

P_AAA77596 1 GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTTGGTGGTGGTGGCTGTTGGG

DNA40981 61 TGCCTTGCAAAAATGAAGGATGCAGGACGCAGCTTTCCTCGGAACCGAACGCAATGGAT

P_AAA77596 61 TGCCTTGCAAAAATGAAGGATGCAGGACGCAGCTTTCCTCGGAACCGAACGCAATGGAT

BLAST RESULTS A-13

DNA40981	121	AAACTGATTGTGCAAGAGAGAAGGAAGAACGAAGCTTTTTCTTGTGAGCCCTGGATCTTA
P_AAA77596	121	AAACTGATTGTGCAAGAGAGAAGGAAGAACGAAGCTTTTTCTTGTGAGCCCTGGATCTTA
DNA40981	181	ACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAATAAACCAGAGTTAGA
P_AAA77596	181	ACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAATAAACCAGAGTTAGA
DNA40981	241	CCCGCGGGGGTTGGTGTGTTCTGACATAAAATAAATAATCTTAAAGCAGCTGTTCCCCCTCC
P_AAA77596	241	CCCGCGGGGGTTGGTGTGTTCTGACATAAAATAAATAATCTTAAAGCAGCTGTTCCCCCTCC
DNA40981	301	CCACCCCCAAAAAAGGATGATTGGAAATGAAGAACCGAGGATTCACAAAGAAAAAAGT
P_AAA77596	301	CCACCCCCAAAAAAGGATGATTGGAAATGAAGAACCGAGGATTCACAAAGAAAAAAGT
DNA40981	361	ATGTTTCATTTTTCTCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTTTGGAATGAAAAG
P_AAA77596	361	ATGTTTCATTTTTCTCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTTTGGAATGAAAAG
DNA40981	421	TTTGGGGCTTTTTTAGTAAAGTAAAGAACTGGTGTGGTGGTGTTTTCCTTTCTTTTTGAA
P_AAA77596	421	TTTGGGGCTTTTTTAGTAAAGTAAAGAACTGGTGTGGTGGTGTTTTCCTTTCTTTTTGAA
DNA40981	481	TTTCCCACAAGAGGAGAGGAAATTAATAATACATCTGCAAAGAAATTCAGAGAAGAAAA
P_AAA77596	481	TTTCCCACAAGAGGAGAGGAAATTAATAATACATCTGCAAAGAAATTCAGAGAAGAAAA
DNA40981	541	GTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACCAGCAGAGCACAGTTGGA
P_AAA77596	541	GTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACCAGCAGAGCACAGTTGGA
DNA40981	601	TTTGTGCCTATGTTGACTAAATTTGACGGATAATTGCAGTTGGATTTTTCTTCATCAACC
P_AAA77596	601	TTTGTGCCTATGTTGACTAAATTTGACGGATAATTGCAGTTGGATTTTTCTTCATCAACC
DNA40981	661	TCCTTTTTTTTTAAATTTTTATTCCTTTTGGTATCAAGATCATGCGTTTTCTCTTGTCTTT
P_AAA77596	661	TCCTTTTTTTTTAAATTTTTATTCCTTTTGGTATCAAGATCATGCGTTTTCTCTTGTCTTT
DNA40981	721	AACCACCTGGATTTCCATCTGGATGTTGCTGTGATCAGTCTGAAATACAACGTGTTTGAAT
P_AAA77596	721	AACCACCTGGATTTCCATCTGGATGTTGCTGTGATCAGTCTGAAATACAACGTGTTTGAAT
DNA40981	781	TCCAGAAGGACCAACACCAGATAAATTATGAATGTTGAACAAGATGACCTTACATCCACA
P_AAA77596	781	TCCAGAAGGACCAACACCAGATAAATTATGAATGTTGAACAAGATGACCTTACATCCACA
DNA40981	841	GCAGATAATGATAGGTCCTAGGTTTAACAGGGCCCTATTTGACCCCCTGCTTGTGGTGGCT
P_AAA77596	841	GCAGATAATGATAGGTCCTAGGTTTAACAGGGCCCTATTTGACCCCCTGCTTGTGGTGGCT
DNA40981	901	GCTGGCTCTTCAACTTCCTTGTGGTGGCTGGTCTGGTGCGGGCTCAGACCTGCCCTTCTGT
P_AAA77596	901	GCTGGCTCTTCAACTTCCTTGTGGTGGCTGGTCTGGTGCGGGCTCAGACCTGCCCTTCTGT
DNA40981	961	GTGCTCCTGCAGCAACCAGTTCAGCAAGGTGATTTGTGTTTCGGAAAAACCTGCGTGAGGT
P_AAA77596	961	GTGCTCCTGCAGCAACCAGTTCAGCAAGGTGATTTGTGTTTCGGAAAAACCTGCGTGAGGT
DNA40981	1021	TCCGGATGGCATCTCCACCAACACACGGCTGCTGAACCTCCATGAGAACC AAAATCCAGAT
P_AAA77596	1021	TCCGGATGGCATCTCCACCAACACACGGCTGCTGAACCTCCATGAGAACC AAAATCCAGAT

BLAST RESULTS A-K

DNA40981	1081	CATCAAAGTGAACAGCTTCAAGCACTTGAGGCACTTGGAATCCTACAGTTGAGTAGGAA
P_AAA77596	1081	CATCAAAGTGAACAGCTTCAAGCACTTGAGGCACTTGGAATCCTACAGTTGAGTAGGAA
DNA40981	1141	CCATATCAGAACCATTGAAATTGGGGCTTTCAATGGTCTGGCGAACCTCAACACTCTGGA
P_AAA77596	1141	CCATATCAGAACCATTGAAATTGGGGCTTTCAATGGTCTGGCGAACCTCAACACTCTGGA
DNA40981	1201	ACTCTTTGACAATCGTCTTACTACCATCCCGAATGGAGCTTTTGTATACTTGTCTAAACT
P_AAA77596	1201	ACTCTTTGACAATCGTCTTACTACCATCCCGAATGGAGCTTTTGTATACTTGTCTAAACT
DNA40981	1261	GAAGGAGCTCTGGTTGCGAAACAACCCCATTTGAAAGCATCCCTTCTTATGCTTTTAACAG
P_AAA77596	1261	GAAGGAGCTCTGGTTGCGAAACAACCCCATTTGAAAGCATCCCTTCTTATGCTTTTAACAG
DNA40981	1321	AATTCCCTTCTTTGCGCCGACTAGACTTAGGGGAATTGAAAAGACTTTCATACATCTCAGA
P_AAA77596	1321	AATTCCCTTCTTTGCGCCGACTAGACTTAGGGGAATTGAAAAGACTTTCATACATCTCAGA
DNA40981	1381	AGGTGCCCTTTGAAGGTCTGTCCAACCTTGAGGTATTTGAACCTTGCCATGTGCAACCTTCG
P_AAA77596	1381	AGGTGCCCTTTGAAGGTCTGTCCAACCTTGAGGTATTTGAACCTTGCCATGTGCAACCTTCG
DNA40981	1441	GGAAATCCCTAACCTCACACCGCTCATAAAC TAGATGAGCTGGATCTTCTGCGAATCA
P_AAA77596	1441	GGAAATCCCTAACCTCACACCGCTCATAAAC TAGATGAGCTGGATCTTCTGCGAATCA
DNA40981	1501	TTTATCTGCCATCAGGCCTGGCTCTTTCCAGGGTTTGATGCACCTTCAAAAAC TGTGGAT
P_AAA77596	1501	TTTATCTGCCATCAGGCCTGGCTCTTTCCAGGGTTTGATGCACCTTCAAAAAC TGTGGAT
DNA40981	1561	GATACAGTCCCAGATTCAAGTGATTGAACGGAATGCCCTTGACAACCTTCAGTCACTAGT
P_AAA77596	1561	GATACAGTCCCAGATTCAAGTGATTGAACGGAATGCCCTTGACAACCTTCAGTCACTAGT
DNA40981	1621	GGAGATCAACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTTCACTCCCTT
P_AAA77596	1621	GGAGATCAACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTTCACTCCCTT
DNA40981	1681	GCATCATCTAGAGCGGATACATTTACATCACAAACCTTGGAACGTAACTGTGACATACT
P_AAA77596	1681	GCATCATCTAGAGCGGATACATTTACATCACAAACCTTGGAACGTAACTGTGACATACT
DNA40981	1741	GTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTTGTGCCCGGTG
P_AAA77596	1741	GTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTTGTGCCCGGTG
DNA40981	1801	TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCAC
P_AAA77596	1801	TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCAC
DNA40981	1861	ATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGC
P_AAA77596	1861	ATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGC
DNA40981	1921	AGCTGAGCTGAAATGTGCGGCCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAA
P_AAA77596	1921	AGCTGAGCTGAAATGTGCGGCCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAA
DNA40981	1981	TGGAACAGTCATGACACATGGGGCGTACAAAGTGCGGATAGCTGTGCTCAGTGATGGTAC
P_AAA77596	1981	TGGAACAGTCATGACACATGGGGCGTACAAAGTGCGGATAGCTGTGCTCAGTGATGGTAC

BLAST RESULTS A-15

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APR 17 2002

TECH CENTER 1600/2900

BLAST RESULTS

DNA40981 2041 GTTAAATTTACAAATGTAAGTGTGCAAGATACAGGCATGTACACATGTATGGTGAGTAA

P_AAA77596 2041 GTTAAATTTACAAATGTAAGTGTGCAAGATACAGGCATGTACACATGTATGGTGAGTAA

DNA40981 2101 TTCCGTTGGGAATACTACTGCTTCAGCCACCCTGAATGTTACTGCAGCAACCACTACTCC

P_AAA77596 2101 TTCCGTTGGGAATACTACTGCTTCAGCCACCCTGAATGTTACTGCAGCAACCACTACTCC

DNA40981 2161 TTTCTCTTACTTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG

P_AAA77596 2161 TTTCTCTTACTTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG

DNA40981 2221 GACCACAGATAACAATGTGGGTCCCAGTCCAGTGGTTCGACTGGGAGACCACCAATGTGAC

P_AAA77596 2221 GACCACAGATAACAATGTGGGTCCCAGTCCAGTGGTTCGACTGGGAGACCACCAATGTGAC

DNA40981 2281 CACCTCTCTCACACCACAGAGCACAAGGTCGACAGAGAAAACCTTCACCATCCCAGTGAC

P_AAA77596 2281 CACCTCTCTCACACCACAGAGCACAAGGTCGACAGAGAAAACCTTCACCATCCCAGTGAC

DNA40981 2341 TGATATAAACAGTGGGATCCCAGGAATTGATGAGGTCATGAAGACTACCAAAATCATCAT

P_AAA77596 2341 TGATATAAACAGTGGGATCCCAGGAATTGATGAGGTCATGAAGACTACCAAAATCATCAT

DNA40981 2401 TGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCATTTTCTACAAGAT

P_AAA77596 2401 TGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCATTTTCTACAAGAT

DNA40981 2461 GAGGAAGCAGCACCATCGGCAAAACCATCACGCCCCAACAAGGACTGTTGAAATTATTAA

P_AAA77596 2461 GAGGAAGCAGCACCATCGGCAAAACCATCACGCCCCAACAAGGACTGTTGAAATTATTAA

DNA40981 2521 TGTGGATGATGAGATTACGGGAGACACACCCATGGAAAGCCACCTGCCCATGCCTGCTAT

P_AAA77596 2521 TGTGGATGATGAGATTACGGGAGACACACCCATGGAAAGCCACCTGCCCATGCCTGCTAT

DNA40981 2581 CGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTTCAACCACACAACAAC

P_AAA77596 2581 CGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTTCAACCACACAACAAC

DNA40981 2641 AGTTAACACAATAAATTCATACACAGTTCAGTGCATGAACCGTTATTGATCCGAATGAA

P_AAA77596 2641 AGTTAACACAATAAATTCATACACAGTTCAGTGCATGAACCGTTATTGATCCGAATGAA

DNA40981 2701 CTCTAAAGACAATGTACAAGAGACTCAAATCTAAAACATTTACAGAGTTACAAAAAACAA

P_AAA77596 2701 CTCTAAAGACAATGTACAAGAGACTCAAATCTAAAACATTTACAGAGTTACAAAAAACAA

DNA40981 2761 ACAATCAAAAAAAAAAGACAGTTTATTAAAAATGACACAAATGACTGGGCTAAATCTACTG

P_AAA77596 2761 ACAATCAAAAAAAAAAGACAGTTTATTAAAAATGACACAAATGACTGGGCTAAATCTACTG

DNA40981 2821 TTTCAAAAAAGTGCTTTTACAAAAAACAAAAAGAAAAGAAATTTATTTATTAAAAATT

P_AAA77596 2821 TTTCAAAAAAGTGCTTTTACAAAAAACAAAAAGAAAAGAAATTTATTTATTAAAAATT

DNA40981 2881 CTATTGTGATCTAAAGCAGACAAAAA

P_AAA77596 2881 CTATTGTGATCTAAAGCAGACAAAAA

>6 P_AAX52265 Protein PRO331 cDNA clone DNA40981-1234. DNA, PAT 25-JUN-1999
(2906 bp) [1 seg]
Score = 2906 (5761 bits), Expect = 0.0

Identities = 2906/2906 (100%), at 1,1-2906,2906, Strand +/-

```
DNA40981      1  GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGG
*****
P_AAX52265    1  GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGG

DNA40981     61  TGCCTTGCAAAAATGAAGGATGCAGGACGCAGCTTTCTCCTGGAACCGAACGCAATGGAT
*****
P_AAX52265    61  TGCCTTGCAAAAATGAAGGATGCAGGACGCAGCTTTCTCCTGGAACCGAACGCAATGGAT

DNA40981    121  AAACGTATTGTGCAAGAGAGAAGGAAGAACGAAGCTTTTTCTTGTGAGCCCTGGATCTTA
*****
P_AAX52265   121  AAACGTATTGTGCAAGAGAGAAGGAAGAACGAAGCTTTTTCTTGTGAGCCCTGGATCTTA

DNA40981    181  ACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAATAAACAGAGTTAGA
*****
P_AAX52265   181  ACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAATAAACAGAGTTAGA

DNA40981    241  CCCGCGGGGGTTGGTGTGTTCTGACATAAATAAATAATCTTAAAGCAGCTGTTCCCCTCC
*****
P_AAX52265   241  CCCGCGGGGGTTGGTGTGTTCTGACATAAATAAATAATCTTAAAGCAGCTGTTCCCCTCC

DNA40981    301  CCACCCCCAAAAAAGGATGATTGGAAATGAAGAACCGAGGATTACAAAGAAAAAAGT
*****
P_AAX52265   301  CCACCCCCAAAAAAGGATGATTGGAAATGAAGAACCGAGGATTACAAAGAAAAAAGT

DNA40981    361  ATGTTTCATTTTCTCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTTGGAAATGAAAAG
*****
P_AAX52265   361  ATGTTTCATTTTCTCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTTGGAAATGAAAAG

DNA40981    421  TTTGGGGCTTTTTTAGTAAAGTAAAGAACTGGTGTGGTGGTGTTCCTTTCTTTTGTAA
*****
P_AAX52265   421  TTTGGGGCTTTTTTAGTAAAGTAAAGAACTGGTGTGGTGGTGTTCCTTTCTTTTGTAA

DNA40981    481  TTTCCCACAAGAGGAGAGGAAATTAATAATACATCTGCAAAGAAATTCAGAGAAGAAAA
*****
P_AAX52265   481  TTTCCCACAAGAGGAGAGGAAATTAATAATACATCTGCAAAGAAATTCAGAGAAGAAAA

DNA40981    541  GTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACCAGCAGAGCACAGTTGGA
*****
P_AAX52265   541  GTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACCAGCAGAGCACAGTTGGA

DNA40981    601  TTTGTGCCTATGTTGACTAAAAATTGACGGATAATTGCAGTTGGATTTTCTTCATCAACC
*****
P_AAX52265   601  TTTGTGCCTATGTTGACTAAAAATTGACGGATAATTGCAGTTGGATTTTCTTCATCAACC

DNA40981    661  TCCTTTTTTTTAAATTTTTATTCCTTTTGGTATCAAGATCATGCGTTTTCTCTTGTTCCT
*****
P_AAX52265   661  TCCTTTTTTTTAAATTTTTATTCCTTTTGGTATCAAGATCATGCGTTTTCTCTTGTTCCT

DNA40981    721  AACCACCTGGATTTCATCTGGATGTTGCTGTGATCAGTCTGAAATACAACGTGTTGAAT
*****
P_AAX52265   721  AACCACCTGGATTTCATCTGGATGTTGCTGTGATCAGTCTGAAATACAACGTGTTGAAT

DNA40981    781  TCCAGAAGGACCAACACCAGATAAATTATGAATGTTGAACAAGATGACCTTACATCCACA
*****
P_AAX52265   781  TCCAGAAGGACCAACACCAGATAAATTATGAATGTTGAACAAGATGACCTTACATCCACA

DNA40981    841  GCAGATAATGATAGGTCCTAGGTTTAAACAGGGCCCTATTTGACCCCTGCTTGTGGTGCT
*****
P_AAX52265   841  GCAGATAATGATAGGTCCTAGGTTTAAACAGGGCCCTATTTGACCCCTGCTTGTGGTGCT

DNA40981    901  GCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGCAGGCTCAGACCTGCCCTTCTGT
*****
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BLAST RESULTS A-17

TECH CENTER 1600/2900

APR 17 2002

P_AAX52265 901 GCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGC GGCTCAGACCTGCCCTTCTGT

DNA40981 961 GTGCTCCTGCAGCAACCAGTTCAGCAAGGTGATTTGTGTTTCGGAAAAACCTGCGTGAGGT

P_AAX52265 961 GTGCTCCTGCAGCAACCAGTTCAGCAAGGTGATTTGTGTTTCGGAAAAACCTGCGTGAGGT

DNA40981 1021 TCCGGATGGCATCTCCACCAACACACGGCTGCTGAACCTCCATGAGAACCAAATCCAGAT

P_AAX52265 1021 TCCGGATGGCATCTCCACCAACACACGGCTGCTGAACCTCCATGAGAACCAAATCCAGAT

DNA40981 1081 CATCAAAGTGAACAGCTTCAAGCACTTGAGGCACTTGGAATCCTACAGTTGAGTAGGAA

P_AAX52265 1081 CATCAAAGTGAACAGCTTCAAGCACTTGAGGCACTTGGAATCCTACAGTTGAGTAGGAA

DNA40981 1141 CCATATCAGAACCATTGAAATTGGGGCTTTCAATGGTCTGGCGAACCTCAACACTCTGGA

P_AAX52265 1141 CCATATCAGAACCATTGAAATTGGGGCTTTCAATGGTCTGGCGAACCTCAACACTCTGGA

DNA40981 1201 ACTCTTTGACAATCGTCTTACTACCATCCCGAATGGAGCTTTTGTATACTTGTCTAAACT

P_AAX52265 1201 ACTCTTTGACAATCGTCTTACTACCATCCCGAATGGAGCTTTTGTATACTTGTCTAAACT

DNA40981 1261 GAAGGAGCTCTGGTTGCGAAACAACCCCATTTGAAAGCATCCCTTCTTATGCTTTTAACAG

P_AAX52265 1261 GAAGGAGCTCTGGTTGCGAAACAACCCCATTTGAAAGCATCCCTTCTTATGCTTTTAACAG

DNA40981 1321 AATTCCTTCTTTGCGCCGACTAGACTTAGGGGAATTGAAAAGACTTTCATACATCTCAGA

P_AAX52265 1321 AATTCCTTCTTTGCGCCGACTAGACTTAGGGGAATTGAAAAGACTTTCATACATCTCAGA

DNA40981 1381 AGGTGCCTTTGAAGGTCTGTCCAACCTTGAGGTATTTGAACCTTGCCATGTGCAACCTTCG

P_AAX52265 1381 AGGTGCCTTTGAAGGTCTGTCCAACCTTGAGGTATTTGAACCTTGCCATGTGCAACCTTCG

DNA40981 1441 GGAAATCCCTAACCTCACACCGCTCATAAACTAGATGAGCTGGATCTTTCTGGGAATCA

P_AAX52265 1441 GGAAATCCCTAACCTCACACCGCTCATAAACTAGATGAGCTGGATCTTTCTGGGAATCA

DNA40981 1501 TTTATCTGCCATCAGGCCCTGGCTCTTTCCAGGGTTTGATGCACCTTCAAAAACCTGTGGAT

P_AAX52265 1501 TTTATCTGCCATCAGGCCCTGGCTCTTTCCAGGGTTTGATGCACCTTCAAAAACCTGTGGAT

DNA40981 1561 GATACAGTCCCAGATTCAAGTGATTGAACGGAATGCCTTTGACAACCTTCAGTCACTAGT

P_AAX52265 1561 GATACAGTCCCAGATTCAAGTGATTGAACGGAATGCCTTTGACAACCTTCAGTCACTAGT

DNA40981 1621 GGAGATCAACCTGGCACACAATAATCTAACATTACTGCCCTCATGACCTCTTCACTCCCTT

P_AAX52265 1621 GGAGATCAACCTGGCACACAATAATCTAACATTACTGCCCTCATGACCTCTTCACTCCCTT

DNA40981 1681 GCATCATCTAGAGCGGATACATTTACATCACAACCTTGGAACCTGTAACCTGTGACATACT

P_AAX52265 1681 GCATCATCTAGAGCGGATACATTTACATCACAACCTTGGAACCTGTAACCTGTGACATACT

DNA40981 1741 GTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTTGTGCCCCGGTG

P_AAX52265 1741 GTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTTGTGCCCCGGTG

DNA40981 1801 TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCAC

P_AAX52265 1801 TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCAC

DNA40981 1861 ATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGC

BLAST RESULTS A-10

APR 17 2002

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P_AAX52265	1861	ATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGC
DNA40981	1921	AGCTGAGCTGAAATGTCGGGCCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAA *****
P_AAX52265	1921	AGCTGAGCTGAAATGTCGGGCCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAA
DNA40981	1981	TGGAACAGTCATGACACATGGGGCGTACAAAGTGC GGATAGCTGTGCTCAGTGATGGTAC *****
P_AAX52265	1981	TGGAACAGTCATGACACATGGGGCGTACAAAGTGC GGATAGCTGTGCTCAGTGATGGTAC
DNA40981	2041	GT TAAATTT CACAAATGTA ACTGTGCAAGATACAGGCATGTACACATGTATGGTGAGTAA *****
P_AAX52265	2041	GT TAAATTT CACAAATGTA ACTGTGCAAGATACAGGCATGTACACATGTATGGTGAGTAA
DNA40981	2101	TTCCGTTGGGAATACTACTTGCTTCAGCCACCCTGAATGTTACTGCAGCAACCACTACTCC *****
P_AAX52265	2101	TTCCGTTGGGAATACTACTTGCTTCAGCCACCCTGAATGTTACTGCAGCAACCACTACTCC
DNA40981	2161	TTTCTCTTACTTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG *****
P_AAX52265	2161	TTTCTCTTACTTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG
DNA40981	2221	GACCACAGATAACAATGTGGGTCCCACTCCAGTGGTTCGACTGGGAGACCACCAATGTGAC *****
P_AAX52265	2221	GACCACAGATAACAATGTGGGTCCCACTCCAGTGGTTCGACTGGGAGACCACCAATGTGAC
DNA40981	2281	CACCTCTCTCACACCACAGAGCACAAGGTGCGACAGAGAAAACCTTCACCATCCCAGTGAC *****
P_AAX52265	2281	CACCTCTCTCACACCACAGAGCACAAGGTGCGACAGAGAAAACCTTCACCATCCCAGTGAC
DNA40981	2341	TGATATAAACAGTGGGATCCCAGGAATTGATGAGGTCATGAAGACTACCAAAATCATCAT *****
P_AAX52265	2341	TGATATAAACAGTGGGATCCCAGGAATTGATGAGGTCATGAAGACTACCAAAATCATCAT
DNA40981	2401	TGGGTGTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCATTTTCTACAAGAT *****
P_AAX52265	2401	TGGGTGTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCATTTTCTACAAGAT
DNA40981	2461	GAGGAAGCAGCACCATCGGCAAAACCATCACGCCCCAACAAAGGACTGTTGAAATTATTAA *****
P_AAX52265	2461	GAGGAAGCAGCACCATCGGCAAAACCATCACGCCCCAACAAAGGACTGTTGAAATTATTAA
DNA40981	2521	TGTGGATGATGAGATTACGGGAGACACACCCATGGAAAGCCACCTGCCCATGCCTGCTAT *****
P_AAX52265	2521	TGTGGATGATGAGATTACGGGAGACACACCCATGGAAAGCCACCTGCCCATGCCTGCTAT
DNA40981	2581	CGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTTCAACCACACAACAAC *****
P_AAX52265	2581	CGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTTCAACCACACAACAAC
DNA40981	2641	AGTTAACACAATAAATTCAATACACAGTTCAGTGCATGAACCGTTATTGATCCGAATGAA *****
P_AAX52265	2641	AGTTAACACAATAAATTCAATACACAGTTCAGTGCATGAACCGTTATTGATCCGAATGAA
DNA40981	2701	CTCTAAAGACAATGTACAAGAGACTCAAATCTAAAACATTTACAGAGTTACAAAAAACAA *****
P_AAX52265	2701	CTCTAAAGACAATGTACAAGAGACTCAAATCTAAAACATTTACAGAGTTACAAAAAACAA
DNA40981	2761	ACAATCAAAAAAAGACAGTTTATTAAAAATGACACAAATGACTGGGCTAAATCTACTG *****
P_AAX52265	2761	ACAATCAAAAAAAGACAGTTTATTAAAAATGACACAAATGACTGGGCTAAATCTACTG
DNA40981	2821	TTTCAAAAAAGTGCTTTTACAAAAAACAAAAAGAAAAGAAATTTATTTATTAAAAATT *****

BLAST RESULTS A-19

TECH CENTER 1600/2900

APR 17 2002

P_AAX52265 2821 TTTCAAAAAAGTGTCTTTACAAAAAACAAGAAATTTATTTATTAATAAATT
DNA40981 2881 CTATTGTGATCTAAAGCAGACAAAAA

P_AAX52265 2881 CTATTGTGATCTAAAGCAGACAAAAA

>7 AX098385 Sequence 11 from Patent W00119991. (2906 bp) [1 seg]
Score = 2906 (5761 bits), Expect = 0.0
Identities = 2906/2906 (100%), at 1,1-2906,2906, Strand +/-

DNA40981 1 GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGG

AX098385 1 GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGG
DNA40981 61 TGCCTTGCAAAAATGAAGGATGCAGGACGCAGCTTTCTCCTGGAACCGAACGCAATGGAT

AX098385 61 TGCCTTGCAAAAATGAAGGATGCAGGACGCAGCTTTCTCCTGGAACCGAACGCAATGGAT
DNA40981 121 AAACGTATTGTGCAAGAGAGAAGGAAGAACGAAGCTTTTTCTTGTGAGCCCTGGATCTTA

AX098385 121 AAACGTATTGTGCAAGAGAGAAGGAAGAACGAAGCTTTTTCTTGTGAGCCCTGGATCTTA
DNA40981 181 ACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAATAAACAGAGTTAGA

AX098385 181 ACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAATAAACAGAGTTAGA
DNA40981 241 CCCGCGGGGTTGGTGTGTTCTGACATAAATAAATAATCTTAAAGCAGCTGTTCCCTCC

AX098385 241 CCCGCGGGGTTGGTGTGTTCTGACATAAATAAATAATCTTAAAGCAGCTGTTCCCTCC
DNA40981 301 CCACCCCAAAAAAAGGATGATTGGAAATGAAGAACCGAGGATTCACAAAGAAAAAGT

AX098385 301 CCACCCCAAAAAAAGGATGATTGGAAATGAAGAACCGAGGATTCACAAAGAAAAAGT
DNA40981 361 ATGTTTCATTTTTCTCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTTTGGAATGAAAAG

AX098385 361 ATGTTTCATTTTTCTCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTTTGGAATGAAAAG
DNA40981 421 TTTGGGGCTTTTTTAGTAAAGTAAAGAACTGGTGTGGTGGTGTTTTTCTTTCTTTTTGAA

AX098385 421 TTTGGGGCTTTTTTAGTAAAGTAAAGAACTGGTGTGGTGGTGTTTTTCTTTCTTTTTGAA
DNA40981 481 TTTCCCACAAGAGGAGAGGAAATTAATAATACATCTGCAAAGAAATTCAGAGAAGAAAA

AX098385 481 TTTCCCACAAGAGGAGAGGAAATTAATAATACATCTGCAAAGAAATTCAGAGAAGAAAA
DNA40981 541 GTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACCAGCAGAGCACAGTTGGA

AX098385 541 GTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACCAGCAGAGCACAGTTGGA
DNA40981 601 TTTGTGCCATATGTTGACTAAAATTGACGGATAATTGCAGTTGGATTTTTCTTCATCAACC

AX098385 601 TTTGTGCCATATGTTGACTAAAATTGACGGATAATTGCAGTTGGATTTTTCTTCATCAACC
DNA40981 661 TCCTTTTTTTTTAAATTTTTATTCCTTTTGGTATCAAGATCATGCGTTTTCTCTTGTTCCTT

AX098385 661 TCCTTTTTTTTTAAATTTTTATTCCTTTTGGTATCAAGATCATGCGTTTTCTCTTGTTCCTT
DNA40981 721 AACCACCTGGATTTCATCTGGATGTTGCTGTGATCAGTCTGAAATACAACGTGTTGAAT

AX098385 721 AACCACCTGGATTTCATCTGGATGTTGCTGTGATCAGTCTGAAATACAACGTGTTGAAT
DNA40981 781 TCCAGAAGGACCAACACCAGATAAATTATGAATGTTGAACAAGATGACCTTACATCCACA

BLAST RESULTS A-20

TECH CENTER 1600/2900

APR 17 2002

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AX098385	781	TCCAGAAGGACCAACACCAGATAAATTATGAATGTTGAACAAGATGACCTTACATCCACA
DNA40981	841	GCAGATAATGATAGGTCTTAGGTTTAACAGGGCCCTATTTGACCCCCTGCTTGTGGTGCT *****
AX098385	841	GCAGATAATGATAGGTCTTAGGTTTAACAGGGCCCTATTTGACCCCCTGCTTGTGGTGCT
DNA40981	901	GCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGCGGGCTCAGACCTGCCCTTCTGT *****
AX098385	901	GCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGCGGGCTCAGACCTGCCCTTCTGT
DNA40981	961	GTGCTCCTGCAGCAACCAGTTCAGCAAGGTGATTTGTGTTCGGAAAAACCTGCGTGAGGT *****
AX098385	961	GTGCTCCTGCAGCAACCAGTTCAGCAAGGTGATTTGTGTTCGGAAAAACCTGCGTGAGGT
DNA40981	1021	TCCGGATGGCATCTCCACCAACACACGGCTGCTGAACCTCCATGAGAACCAAATCCAGAT *****
AX098385	1021	TCCGGATGGCATCTCCACCAACACACGGCTGCTGAACCTCCATGAGAACCAAATCCAGAT
DNA40981	1081	CATCAAAGTGAACAGCTTCAAGCAC'TTGAGGCAC'TTGGAATCC'TACAGTTGAGTAGGAA *****
AX098385	1081	CATCAAAGTGAACAGCTTCAAGCAC'TTGAGGCAC'TTGGAATCC'TACAGTTGAGTAGGAA
DNA40981	1141	CCATATCAGAACCATTGAAATTTGGGGCTTTCAATGGTCTGGCGAACCTCAACACTCTGGA *****
AX098385	1141	CCATATCAGAACCATTGAAATTTGGGGCTTTCAATGGTCTGGCGAACCTCAACACTCTGGA
DNA40981	1201	ACTCTTTGACAATCGTCTTACTACCATCCCGAATGGAGCTTTTGTATACCTTGTCTAAACT *****
AX098385	1201	ACTCTTTGACAATCGTCTTACTACCATCCCGAATGGAGCTTTTGTATACCTTGTCTAAACT
DNA40981	1261	GAAGGAGCTCTGGTTGCGAAACAACCCCATTTGAAAGCATCCCTTCTTATGCTTTTAACAG *****
AX098385	1261	GAAGGAGCTCTGGTTGCGAAACAACCCCATTTGAAAGCATCCCTTCTTATGCTTTTAACAG
DNA40981	1321	AATTCCTTCTTTGCGCCGACTAGACTTAGGGGAATTGAAAAGACTTTTCATACATCTCAGA *****
AX098385	1321	AATTCCTTCTTTGCGCCGACTAGACTTAGGGGAATTGAAAAGACTTTTCATACATCTCAGA
DNA40981	1381	AGGTGCCCTTTGAAGGTCTGTCCAACCTTGAGGTATTTGAACCTTGCCATGTGCAACCTTCG *****
AX098385	1381	AGGTGCCCTTTGAAGGTCTGTCCAACCTTGAGGTATTTGAACCTTGCCATGTGCAACCTTCG
DNA40981	1441	GGAAATCCCTAACCTCACACCGCTCATAAAACTAGATGAGCTGGATCTTTCTGGGAATCA *****
AX098385	1441	GGAAATCCCTAACCTCACACCGCTCATAAAACTAGATGAGCTGGATCTTTCTGGGAATCA
DNA40981	1501	TTTATCTGCCATCAGGCCTGGCTCTTTCCAGGGTTTGATGCACCTTCAAAAACTGTGGAT *****
AX098385	1501	TTTATCTGCCATCAGGCCTGGCTCTTTCCAGGGTTTGATGCACCTTCAAAAACTGTGGAT
DNA40981	1561	GATACAGTCCCAGATTCAAGTGATTGAACGGAATGCCTTTGACAACCTTCAGTCACTAGT *****
AX098385	1561	GATACAGTCCCAGATTCAAGTGATTGAACGGAATGCCTTTGACAACCTTCAGTCACTAGT
DNA40981	1621	GGAGATCAACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTTCACTCCCTT *****
AX098385	1621	GGAGATCAACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTTCACTCCCTT
DNA40981	1681	GCATCATCTAGAGCGGATACATTTACATCACAACCCTTGGAAGTGTAAGTGTGACATACT *****
AX098385	1681	GCATCATCTAGAGCGGATACATTTACATCACAACCCTTGGAAGTGTAAGTGTGACATACT
DNA40981	1741	GTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTTGTGCCCGGTG *****

BLAST RESULTS A-21

TECH CENTER 1600/2900

APR 17 2002

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AX098385	1741	GTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTGTGCCCCGGTG
DNA40981	1801	TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCAC *****
AX098385	1801	TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCAC
DNA40981	1861	ATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGC *****
AX098385	1861	ATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGC
DNA40981	1921	AGCTGAGCTGAAATGTCGGGCCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAA *****
AX098385	1921	AGCTGAGCTGAAATGTCGGGCCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAA
DNA40981	1981	TGGAACAGTCATGACACATGGGGCGTACAAAGTGCGGATAGCTGTGCTCAGTGATGGTAC *****
AX098385	1981	TGGAACAGTCATGACACATGGGGCGTACAAAGTGCGGATAGCTGTGCTCAGTGATGGTAC
DNA40981	2041	GTAAATTTACAAAATGTAAGTGTGCAAGATACAGGCATGTACACATGTATGGTGAGTAA *****
AX098385	2041	GTAAATTTACAAAATGTAAGTGTGCAAGATACAGGCATGTACACATGTATGGTGAGTAA
DNA40981	2101	TTCCGTTGGGAATACTACTGCTTCAGCCACCCTGAATGTTACTGCAGCAACCACTACTCC *****
AX098385	2101	TTCCGTTGGGAATACTACTGCTTCAGCCACCCTGAATGTTACTGCAGCAACCACTACTCC
DNA40981	2161	TTTCTCTTACTTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG *****
AX098385	2161	TTTCTCTTACTTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG
DNA40981	2221	GACCACAGATAACAATGTGGGTCCCCTCCAGTGGTTCGACTGGGAGACCACCAATGTGAC *****
AX098385	2221	GACCACAGATAACAATGTGGGTCCCCTCCAGTGGTTCGACTGGGAGACCACCAATGTGAC
DNA40981	2281	CACCTCTCTCACACCACAGAGCACAAGGTCGACAGAGAAAACCTTCACCATCCCAGTGAC *****
AX098385	2281	CACCTCTCTCACACCACAGAGCACAAGGTCGACAGAGAAAACCTTCACCATCCCAGTGAC
DNA40981	2341	TGATATAAACAGTGGGATCCCAGGAATTGATGAGGTCATGAAGACTACCAAAATCATCAT *****
AX098385	2341	TGATATAAACAGTGGGATCCCAGGAATTGATGAGGTCATGAAGACTACCAAAATCATCAT
DNA40981	2401	TGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCATTTTCTACAAGAT *****
AX098385	2401	TGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCATTTTCTACAAGAT
DNA40981	2461	GAGGAAGCAGCACCATCGGCAAAACCATCACGCCCCAACAAGGACTGTTGAAATTATTAA *****
AX098385	2461	GAGGAAGCAGCACCATCGGCAAAACCATCACGCCCCAACAAGGACTGTTGAAATTATTAA
DNA40981	2521	TGTGGATGATGAGATTACGGGAGACACACCCATGGAAAGCCACCTGCCCATGCCGTGCTAT *****
AX098385	2521	TGTGGATGATGAGATTACGGGAGACACACCCATGGAAAGCCACCTGCCCATGCCGTGCTAT
DNA40981	2581	CGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTTCAACCACACAACAAC *****
AX098385	2581	CGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTTCAACCACACAACAAC
DNA40981	2641	AGTTAACACAATAAATTCAATACACAGTTCAGTGCATGAACCGTTATTGATCCGAATGAA *****
AX098385	2641	AGTTAACACAATAAATTCAATACACAGTTCAGTGCATGAACCGTTATTGATCCGAATGAA
DNA40981	2701	CTCTAAAGACAATGTACAAGAGACTCAAATCTAAAACATTTACAGAGTTACAAAAAACAA *****

TECH CENTER 1600/2900

APR 17 2002

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BLAST RESULTS A-22

AX098385 2701 CTCTAAAGACAATGTACAAGAGACTCAAATCTAAAACATTTACAGAGTTACAAAAAACAA
DNA40981 2761 ACAATCAAAAAAAAAAAGACAGTTTATTAATAAATGACACAAATGACTGGGCTAAATCTACTG

AX098385 2761 ACAATCAAAAAAAAAAAGACAGTTTATTAATAAATGACACAAATGACTGGGCTAAATCTACTG
DNA40981 2821 TTTCAAAAAAGTGTCTTTACAAAAAACAAAAAGAAAAGAAATTTATTTATTAAAAATT

AX098385 2821 TTTCAAAAAAGTGTCTTTACAAAAAACAAAAAGAAAAGAAATTTATTTATTAAAAATT
DNA40981 2881 CTATTGTGATCTAAAGCAGACAAAAA

AX098385 2881 CTATTGTGATCTAAAGCAGACAAAAA

>8 AB046800 Homo sapiens mRNA for KIAA1580 protein, partial cds. (4055 bp) [1 seg]

Score = 2889 (5727 bits), Expect = 0.0

Identities = 2898/2901 (99%), at 1,1155-2901,4055, Strand +/-

DNA40981 1 GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGG

AB046800 1155 GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGG
DNA40981 61 TGCCTTGCAAAAATGAAGGATGCAGGACGCAGCTTCTCCTGGAACCGAACGCAATGGAT

AB046800 1215 TGCCTTGCAAAAATGAAGGATGCAGGACGCAGCTTCTCCTGGAACCGAACGCAATGGAT
DNA40981 121 AAACGTATTGTGCAAGAGAGAAGGAAGAACGAAGCTTTTTCTTGAGCCCTGGATCTTA

AB046800 1275 AAACGTATTGTGCAAGAGAGAAGGAAGAACGAAGCTTTTTCTTGAGCCCTGGATCTTA
DNA40981 181 ACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAATAAACAGAGTTAGA

AB046800 1335 ACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAATAAACAGAGTTAGA
DNA40981 241 CCCGCGGGGGTTGGTGTGTTCTGACATAAATAAATAATCTTAAAGCAGCTGT'TCCCCTCC

AB046800 1395 CCCGCGGGGGTTGGTGTGTTCTGACATAAATAAATAATCTTAAAGCAGCTGT'TCCCCTCC
DNA40981 301 CCACCCCCAAAAAAGGATGATTGGAAATGAAGAACCGAGGATTACAAAAGAAAAAGT
** *****
AB046800 1455 CCCCCCCCCAAAAAAGGATGATTGGAAATGAAGAACCGAGGATTACAAAAGAAAAAGT
DNA40981 361 ATGTTTCATTTTTCTCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTTTGGAATGAAAAG

AB046800 1515 ATGTTTCATTTTTCTCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTTTGGAATGAAAAG
DNA40981 421 TTTGGGGCTTTTTTAGTAAAGTAAAGAACTGGTGTGGTGGTGT'TTCTTTCTTTTGA

AB046800 1575 TTTGGGGCTTTTTTAGTAAAGTAAAGAACTGGTGTGGTGGTGT'TTCTTTCTTTTGA
DNA40981 481 TTTCCCACAAGAGGAGAGGAAATTAATAATACATCTGCAAAGAAATTTAGAGAGAAAAA

AB046800 1635 TTTCCCACAAGAGGAGAGGAAATTAATAATACATCTGCAAAGAAATTTAGAGAGAAAAA
DNA40981 541 GTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACCAGCAGAGCACAGTTGGA

AB046800 1695 GTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACCAGCAGAGCACAGTTGGA
DNA40981 601 TTTGTGCCTATGTTGACTAAAATTGACGGATAATTGCAGTTGGATTTTTCTTCATCAACC

AB046800 1755 TTTGTGCCTATGTTGACTAAAATTGACGGATAATTGCAGTTGGATTTTTCTTCATCAACC
DNA40981 661 TCCTTTTTTTTAAATTTTTATTCCTTTTGGTATCAAGATCATGCGTTTTCTCTTGTCTT

TECH CENTER 1600/2900

APR 17 2002

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BLAST RESULTS A-23

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*****
AB046800 1815 TCCTTTTTTTTAAATTTTATTCCTTTTGGTATCAAGATCATGCGTTTTCTCTTGTTCTT
DNA40981 721 AACCACCTGGATTTCCATCTGGATGTTGCTGTGATCAGTCTGAAATACAACCTGTTTGAAT
*****
AB046800 1875 AACCACCTGGATTTCCATCTGGATGTTGCTGTGATCAGTCTGAAATACAACCTGTTTGAAT
DNA40981 781 TCCAGAAGGACCAACACCAGATAAATTATGAATGTTGAACAAGATGACCTTACATCCACA
*****
AB046800 1935 TCCAGAAGGACCAACACCAGATAAATTATGAATGTTGAACAAGATGACCTTACATCCACA
DNA40981 841 GCAGATAATGATAGGTCTTAGGTTTAAACAGGGCCCTATTTGACCCCTGCTTGTGGTGGT
*****
AB046800 1995 GCAGATAATGATAGGTCTTAGGTTTAAACAGGGCCCTATTTGACCCCTGCTTGTGGTGGT
DNA40981 901 GCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGC GGGCTCAGACCTGCCCTTCTGT
*****
AB046800 2055 GCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGC GGGCTCAGACCTGCCCTTCTGT
DNA40981 961 GTGCTCCTGTCAGCAACCAGTTCAGCAAGGTGATTTGTGTTTCGGA AAAACCTGCGTGAGGT
*****
AB046800 2115 GTGCTCCTGTCAGCAACCAGTTCAGCAAGGTGATTTGTGTTTCGGA AAAACCTGCGTGAGGT
DNA40981 1021 TCCGGATGGCATCTCCACCAACACACGGCTGC TGAACCTCCATGAGAACCAAATCCAGAT
*****
AB046800 2175 TCCGGATGGCATCTCCACCAACACACGGCTGC TGAACCTCCATGAGAACCAAATCCAGAT
DNA40981 1081 CATCAAAGTGAACAGCTTCAAGCAC TTGAGGCAC TTGGAATCCTACAGTTGAGTAGGAA
*****
AB046800 2235 CATCAAAGTGAACAGCTTCAAGCAC TTGAGACAC TTGGAATCCTACAGTTGAGTAGGAA
DNA40981 1141 CCATATCAGAACCATTGAAATTGGGGCTTTCAATGGTCTGGCGAACCTCAACACTCTGGA
*****
AB046800 2295 CCATATCAGAACCATTGAAATTGGGGCTTTCAATGGTCTGGCGAACCTCAACACTCTGGA
DNA40981 1201 ACTCTTTTGACAATCGTCTTACTACCATCCCCGAATGGAGCTTTTGTATAC TTGTCTAAACT
*****
AB046800 2355 ACTCTTTTGACAATCGTCTTACTACCATCCCCGAATGGAGCTTTTGTATAC TTGTCTAAACT
DNA40981 1261 GAAGGAGCTCTGGTTGCGAAACAACCCCAT TGAAAGCATCCCTTCTTATGCTTTTAAACAG
*****
AB046800 2415 GAAGGAGCTCTGGTTGCGAAACAACCCCAT TGAAAGCATCCCTTCTTATGCTTTTAAACAG
DNA40981 1321 AATTCCTTCTTTGCGCCGACTAGACTTAGGGGAATTGAAAAGACTTTCATACATCTCAGA
*****
AB046800 2475 AATTCCTTCTTTGCGCCGACTAGACTTAGGGGAATTGAAAAGACTTTCATACATCTCAGA
DNA40981 1381 AGGTGCCCTTTGAAGGTCTGTCCAAC TTGAGGTATTTGAACCTTGCCATGTGCAACCTTCG
*****
AB046800 2535 AGGTGCCCTTTGAAGGTCTGTCCAAC TTGAGGTATTTGAACCTTGCCATGTGCAACCTTCG
DNA40981 1441 GGAAATCCCTAACCTCACACCGCTCATAAACTAGATGAGCTGGATCTTTCTGGGAATCA
*****
AB046800 2595 GGAAATCCCTAACCTCACACCGCTCATAAACTAGATGAGCTGGATCTTTCTGGGAATCA
DNA40981 1501 TTTATCTGCCATCAGGCCTGGCTCTTTCCAGGGTTTGATGCACCTTCAAAA ACTGTGGAT
*****
AB046800 2655 TTTATCTGCCATCAGGCCTGGCTCTTTCCAGGGTTTGATGCACCTTCAAAA ACTGTGGAT
DNA40981 1561 GATACAGTCCCAGATTCAAGTGATTGAACGGAATGCCTTTGACAACCTTCAGTCACTAGT
*****
AB046800 2715 GATACAGTCCCAGATTCAAGTGATTGAACGGAATGCCTTTGACAACCTTCAGTCACTAGT
DNA40981 1621 GGAGATCAACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTTCACTCCCTT

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TECH CENTER 1600/2900

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BLAST RESULTS A-24


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*****
AB046800 2775 GGAGATCAACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTTCACTCCCTT
DNA40981 1681 GCATCATCTAGAGCGGATACATTTACATCACAACCCTTGGAAGTGTAACTGTGACATACT
*****
AB046800 2835 GCATCATCTAGAGCGGATACATTTACATCACAACCCTTGGAAGTGTAACTGTGACATACT
DNA40981 1741 GTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTTGTGCCCGGTG
*****
AB046800 2895 GTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTTGTGCCCGGTG
DNA40981 1801 TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCAC
*****
AB046800 2955 TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCAC
DNA40981 1861 ATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACCTGAAGGCATGGC
*****
AB046800 3015 ATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACCTGAAGGCATGGC
DNA40981 1921 AGCTGAGCTGAAATGTCGGGGCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAA
*****
AB046800 3075 AGCTGAGCTGAAATGTCGGGGCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAA
DNA40981 1981 TGGAACAGTCATGACACATGGGGCGTACAAAGTGC GGATAGCTGTGCTCAGTGATGGTAC
*****
AB046800 3135 TGGAACAGTCATGACACATGGGGCGTACAAAGTGC GGATAGCTGTGCTCAGTGATGGTAC
DNA40981 2041 GTTAAATTTACAAAATGTAACCTGTGCAAGATACAGGCATGTACACATGTATGGTGAGTAA
*****
AB046800 3195 GTTAAATTTACAAAATGTAACCTGTGCAAGATACAGGCATGTACACATGTATGGTGAGTAA
DNA40981 2101 TTCCGTTGGGAATACTACTGCTTCAGCCACCCTGAATGTTACTGCAGCAACCCTACTCC
*****
AB046800 3255 TTCCGTTGGGAATACTACTGCTTCAGCCACCCTGAATGTTACTGCAGCAACCCTACTCC
DNA40981 2161 TTTCTCTTACTTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG
*****
AB046800 3315 TTTCTCTTACTTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG
DNA40981 2221 GACCACAGATAACAATGTGGGTCCCACTCCAGTGGTCTGACTGGGAGACCACCAATGTGAC
*****
AB046800 3375 GACCACAGATAACAATGTGGGTCCCACTCCAGTGGTCTGACTGGGAGACCACCAATGTGAC
DNA40981 2281 CACCTCTCTCACACCACAGAGCACAAGGTCGACAGAGAAAACCTTCACCATCCCAGTGAC
*****
AB046800 3435 CACCTCTCTCACACCACAGAGCACAAGGTCGACAGAGAAAACCTTCACCATCCCAGTGAC
DNA40981 2341 TGATATAAACAGTGGGATCCCAGGAATTGATGAGGTCATGAAGACTACCAAAATCATCAT
*****
AB046800 3495 TGATATAAACAGTGGGATCCCAGGAATTGATGAGGTCATGAAGACTACCAAAATCATCAT
DNA40981 2401 TGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCATTTTCTACAAGAT
*****
AB046800 3555 TGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCATTTTCTACAAGAT
DNA40981 2461 GAGGAAGCAGCACCATCGGCAAAACCATCACGCCCCAACAAGGACTGTTGAAATTATTAA
*****
AB046800 3615 GAGGAAGCAGCACCATCGGCAAAACCATCACGCCCCAACAAGGACTGTTGAAATTATTAA
DNA40981 2521 TGTGGATGATGAGATTACGGGAGACACACCCATGGAAAGCCACCTGCCCATGCCTGCTAT
*****
AB046800 3675 TGTGGATGATGAGATTACGGGAGACACACCCATGGAAAGCCACCTGCCCATGCCTGCTAT
DNA40981 2581 CGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTTCAACCACACAACAAC

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BLAST RESULTS A-25

TECH CENTER 1600/2900

APR 17 2002

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*****
AB046800 3735 CGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTTCAACCACACAACAAC
DNA40981 2641 AGTTAACACAATAAATTCAATACACAGTTTCAGTGCATGAACCGTTATTGATCCGAATGAA
*****
AB046800 3795 AGTTAACACAATAAATTCAATACACAGTTTCAGTGCATGAACCGTTATTGATCCGAATGAA
DNA40981 2701 CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTTACAGAGTTACAAAAAACAA
*****
AB046800 3855 CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTTACAGAGTTACAAAAAACAA
DNA40981 2761 ACAATCAAAAAAAGACAGTTTATTAAAAATGACACAAATGACTGGGCTAAATCTACTG
*****
AB046800 3915 ACAATCAAAAAAAGACAGTTTATTAAAAATGACACAAATGACTGGGCTAAATCTACTG
DNA40981 2821 TTTCAAAAAAGTGTCTTTACAAAAAACAAAAAGAAAAGAAATTTATTTATTAAAAATT
*****
AB046800 3975 TTTCAAAAAAGTGTCTTTACAAAAAACAAAAAGAAAAGAAATTTATTTATTAAAAATT
DNA40981 2881 CTATTGTGATCTAAAGCAGAC
*****
AB046800 4035 CTATTGTGATCTAAAGCAGAC

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>9 AC021820 Homo sapiens clone RP11-40H19, WORKING DRAFT SEQUENCE, 11 unordered (157201 bp) [1 seg]
Score = 2136 (4234 bits), Expect = 0.0
Identities = 2136/2136 (100%), at 770,28891-2905,31026, Strand +/-

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DNA40981 770 ACTGTTTGAATTCCAGAAGGACCAACACCAGATAAATTATGAATGTTGAACAAGATGACC
*****
AC021820 28891 ACTGTTTGAATTCCAGAAGGACCAACACCAGATAAATTATGAATGTTGAACAAGATGACC
DNA40981 830 TTACATCCACAGCAGATAATGATAGGTCC TAGGTTTAACAGGGCCCTATTTGACCCCTG
*****
AC021820 28951 TTACATCCACAGCAGATAATGATAGGTCC TAGGTTTAACAGGGCCCTATTTGACCCCTG
DNA40981 890 CTTGTGGTGCCTGCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGCAGGCTCAGACC
*****
AC021820 29011 CTTGTGGTGCCTGCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGCAGGCTCAGACC
DNA40981 950 TGCCCTTCTGTGTGCTCCTGCAGCAACCAGTTCAGCAAGGTGATTTGTGTTTCGGAACAAAC
*****
AC021820 29071 TGCCCTTCTGTGTGCTCCTGCAGCAACCAGTTCAGCAAGGTGATTTGTGTTTCGGAACAAAC
DNA40981 1010 CTGCGTGAGGTTCCGGATGGCATCTCCACCAACACACGGCTGCTGAACCTCCATGAGAAC
*****
AC021820 29131 CTGCGTGAGGTTCCGGATGGCATCTCCACCAACACACGGCTGCTGAACCTCCATGAGAAC
DNA40981 1070 CAAATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAGGCACTTGGAATCCTACAG
*****
AC021820 29191 CAAATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAGGCACTTGGAATCCTACAG
DNA40981 1130 TTGAGTAGGAACCATATCAGAACCATTGAAATTGGGGCTTTCAATGGTCTGGCGAACCTC
*****
AC021820 29251 TTGAGTAGGAACCATATCAGAACCATTGAAATTGGGGCTTTCAATGGTCTGGCGAACCTC
DNA40981 1190 AACACTCTGGAACCTCTTTGACAAATCGTCTTACTACCATCCCCGAATGGAGCTTTTGTATAC
*****
AC021820 29311 AACACTCTGGAACCTCTTTGACAAATCGTCTTACTACCATCCCCGAATGGAGCTTTTGTATAC
DNA40981 1250 TTGTCTAAACTGAAGGAGCTCTGGTTGCGAAACAACCCCATTGAAAGCATCCCTTCTTAT
*****
AC021820 29371 TTGTCTAAACTGAAGGAGCTCTGGTTGCGAAACAACCCCATTGAAAGCATCCCTTCTTAT

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BLAST RESULTS A-24

TECH CENTER 1600/2900

APR 17 2002

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DNA40981	1310	GCTTTTAAACAGAATTCCTTCTTTGCGCCGACTAGACTTAGGGGAATTGAAAAGACTTTCA
AC021820	29431	GCTTTTAAACAGAATTCCTTCTTTGCGCCGACTAGACTTAGGGGAATTGAAAAGACTTTCA
DNA40981	1370	TACATCTCAGAAGGTGCCTTTGAAGGTCTGTCCAACCTTGAGGTATTTGAACCTTGCCATG
AC021820	29491	TACATCTCAGAAGGTGCCTTTGAAGGTCTGTCCAACCTTGAGGTATTTGAACCTTGCCATG
DNA40981	1430	TGCAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAAACTAGATGAGCTGGATCTT
AC021820	29551	TGCAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAAACTAGATGAGCTGGATCTT
DNA40981	1490	TCTGGGAATCATTATCTGCCATCAGGCCTGGCTCTTCCAGGGTTTGATGCACCTTCAA
AC021820	29611	TCTGGGAATCATTATCTGCCATCAGGCCTGGCTCTTCCAGGGTTTGATGCACCTTCAA
DNA40981	1550	AAACTGTGGATGATACAGTCCCAGATTCAAGTGATTGAACGGAATGCCTTTGACAACCTT
AC021820	29671	AAACTGTGGATGATACAGTCCCAGATTCAAGTGATTGAACGGAATGCCTTTGACAACCTT
DNA40981	1610	CAGTCACTAGTGGAGATCAACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTC
AC021820	29731	CAGTCACTAGTGGAGATCAACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTC
DNA40981	1670	TTCAC'TCCCTTGCATCATCTAGAGCGGATACATTTACATCACAACCC'TTGGAACTGTAAC
AC021820	29791	TTCAC'TCCCTTGCATCATCTAGAGCGGATACATTTACATCACAACCC'TTGGAACTGTAAC
DNA40981	1730	TGTGACATACTGTGGCTCAGCTGGTGGATAAAAAGACATGGCCCCCTCGAACACAGCTTGT
AC021820	29851	TGTGACATACTGTGGCTCAGCTGGTGGATAAAAAGACATGGCCCCCTCGAACACAGCTTGT
DNA40981	1790	TGTGCCCCGGTGTAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAG
AC021820	29911	TGTGCCCCGGTGTAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAG
DNA40981	1850	AATTACTTCACATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACT
AC021820	29971	AATTACTTCACATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACT
DNA40981	1910	GAAGGCATGGCAGCTGAGCTGAAATGTCGGGCCTCCACATCCCTGACATCTGTATCTTGG
AC021820	30031	GAAGGCATGGCAGCTGAGCTGAAATGTCGGGCCTCCACATCCCTGACATCTGTATCTTGG
DNA40981	1970	ATTACTCCAAATGGAACAGTCATGACACATGGGGCGTACAAAGTGCGGATAGCTGTGCTC
AC021820	30091	ATTACTCCAAATGGAACAGTCATGACACATGGGGCGTACAAAGTGCGGATAGCTGTGCTC
DNA40981	2030	AGTGATGGTACGTTAAATTTACACAAATGTAAGTGTGCAAGATACAGGCATGTACACATGT
AC021820	30151	AGTGATGGTACGTTAAATTTACACAAATGTAAGTGTGCAAGATACAGGCATGTACACATGT
DNA40981	2090	ATGGTGAGTAATTCCGTTGGGAATACTACTGCTTCAGCCACCCTGAATGTTACTGCAGCA
AC021820	30211	ATGGTGAGTAATTCCGTTGGGAATACTACTGCTTCAGCCACCCTGAATGTTACTGCAGCA
DNA40981	2150	ACCACTACTCCTTTCTCTTACTTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAG
AC021820	30271	ACCACTACTCCTTTCTCTTACTTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAG
DNA40981	2210	GATGAGGCACGGACCACAGATAACAATGTGGGTCCCACTCCAGTGGTTCGACTGGGAGACC
AC021820	30331	GATGAGGCACGGACCACAGATAACAATGTGGGTCCCACTCCAGTGGTTCGACTGGGAGACC

BLAST RESULTS A-27

TECH CENTER 1600/2900

APR 17 2002

DNA40981 2270 ACCAATGTGACCACCTCTCTCACACCACAGAGCACAAGGTCGACAGAGAAAACCTTCACC

 AC021820 30391 ACCAATGTGACCACCTCTCTCACACCACAGAGCACAAGGTCGACAGAGAAAACCTTCACC
 DNA40981 2330 ATCCCAAGTGAAGTATATAAAGAGTGGGATCCCAGGAATTGATGAGGTCATGAAGACTACC

 AC021820 30451 ATCCCAAGTGAAGTATATAAAGAGTGGGATCCCAGGAATTGATGAGGTCATGAAGACTACC
 DNA40981 2390 AAAATCATCATTGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCATT

 AC021820 30511 AAAATCATCATTGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCATT
 DNA40981 2450 TTCTACAAGATGAGGAAGCAGCACCATCGGCAAAACCATCACGCCCCAACAAGGACTGTT

 AC021820 30571 TTCTACAAGATGAGGAAGCAGCACCATCGGCAAAACCATCACGCCCCAACAAGGACTGTT
 DNA40981 2510 GAAATTATTAATGTGGATGATGAGATTACGGGAGACACACCCATGGAAAGCCACCTGCC

 AC021820 30631 GAAATTATTAATGTGGATGATGAGATTACGGGAGACACACCCATGGAAAGCCACCTGCC
 DNA40981 2570 ATGCCCTGCTATCGAGCATGAGCACCTAAATCACTATAAATCATAAAATCTCCCTTCAAC

 AC021820 30691 ATGCCCTGCTATCGAGCATGAGCACCTAAATCACTATAAATCATAAAATCTCCCTTCAAC
 DNA40981 2630 CACACAACAACAGTTAACACAATAAATTCAATACACAGTTTCAGTGCATGAACCGTTATTG

 AC021820 30751 CACACAACAACAGTTAACACAATAAATTCAATACACAGTTTCAGTGCATGAACCGTTATTG
 DNA40981 2690 ATCCGAATGAACCTCTAAAGACAATGTACAAGAGACTCAAATCTAAAACATTTACAGAGTT

 AC021820 30811 ATCCGAATGAACCTCTAAAGACAATGTACAAGAGACTCAAATCTAAAACATTTACAGAGTT
 DNA40981 2750 ACAAAAAACAACAATCAAAAAAAGACAGTTTATTAAAAATGACACAAATGACTGGGC

 AC021820 30871 ACAAAAAACAACAATCAAAAAAAGACAGTTTATTAAAAATGACACAAATGACTGGGC
 DNA40981 2810 TAAATCTACTGTTTCAAAAAAGTGCTTTTACAAAAAACAAAAAGAAAAGAAATTTATT

 AC021820 30931 TAAATCTACTGTTTCAAAAAAGTGCTTTTACAAAAAACAAAAAGAAAAGAAATTTATT
 DNA40981 2870 TATTAAAAATCTATTGTGATCTAAAGCAGACAAA

 AC021820 30991 TATTAAAAATCTATTGTGATCTAAAGCAGACAAA

>10 AC080100 Homo sapiens chromosome 11 clone RP11-454H19 map 11, WORKING DRAFT
 (151999 bp) [1 seg]
 Score = 2132 (4226 bits), Expect = 0.0
 Identities = 2135/2136 (99%), at 770,22645-2905,20510, Strand +/-

DNA40981 770 ACTGTTTGAATTCCAGAAGGACCAACACCAGATAAATTATGAATGTTGAACAAGATGACC

 AC080100 22645 ACTGTTTGAATTCCAGAAGGACCAACACCAGATAAATTATGAATGTTGAACAAGATGACC
 DNA40981 830 TTACATCCACAGCAGATAATGATAGGTCCTAGGTTTAACAGGGCCCTATTTGACCCCTG

 AC080100 22585 TTACATCCACAGCAGATAATGATAGGTCCTAGGTTTAACAGGGCCCTATTTGACCCCTG
 DNA40981 890 CTTGTGGTGGCTGCTGGCTCTTCAACTTCTTGTGGTGGCTGGCTGGTGCAGGCTCAGACC

 AC080100 22525 CTTGTGGTGGCTGCTGGCTCTTCAACTTCTTGTGGTGGCTGGCTGGTGCAGGCTCAGACC
 DNA40981 950 TGCCCTTCTGTGTGCTCCTGCAGCAACCAGTTCAGCAAGGTGATTTGTGTTTCGGAAAAAC

 AC080100 22465 TGCCCTTCTGTGTGCTCCTGCAGCAACCAGTTCAGCAAGGTGATTTGTGTTTCGGAAAAAC

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BLAST RESULTS A-28

DNA40981 1010 CTGCGTGAGGTTCCGGATGGCATCTCCACCAACACACGGCTGCTGAACCTCCATGAGAAC

AC080100 22405 CTGCGTGAGGTTCCGGATGGCATCTCCACCAACACACGGCTGCTGAACCTCCATGAGAAC
DNA40981 1070 CAAATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAGGCACTTGGAATCCTACAG

AC080100 22345 CAAATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAGACACTTGGAATCCTACAG
DNA40981 1130 TTGAGTAGGAACCATATCAGAACCATTGAAATTGGGGCTTTCAATGGTCTGGCGAACCTC

AC080100 22285 TTGAGTAGGAACCATATCAGAACCATTGAAATTGGGGCTTTCAATGGTCTGGCGAACCTC
DNA40981 1190 AACACTCTGGAACCTCTTTGACAATCGTCTTACTACCATCCCGAATGGAGCTTTTGTATAC

AC080100 22225 AACACTCTGGAACCTCTTTGACAATCGTCTTACTACCATCCCGAATGGAGCTTTTGTATAC
DNA40981 1250 TTGTCTAAACTGAAGGAGCTCTGGTTGCGAAACAACCCCATTTGAAAGCATCCCTTCTTAT

AC080100 22165 TTGTCTAAACTGAAGGAGCTCTGGTTGCGAAACAACCCCATTTGAAAGCATCCCTTCTTAT
DNA40981 1310 GCTTTTAAACAGAATTTCCTTCTTTGCGCCGACTAGACTTAGGGGAATTGAAAAGACTTTCA

AC080100 22105 GCTTTTAAACAGAATTTCCTTCTTTGCGCCGACTAGACTTAGGGGAATTGAAAAGACTTTCA
DNA40981 1370 TACATCTCAGAAGGTGCCTTTGAAGGTCTGTCCAACCTTGAGGTATTTGAACCTTGCCATG

AC080100 22045 TACATCTCAGAAGGTGCCTTTGAAGGTCTGTCCAACCTTGAGGTATTTGAACCTTGCCATG
DNA40981 1430 TGCAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAACTAGATGAGCTGGATCTT

AC080100 21985 TGCAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAACTAGATGAGCTGGATCTT
DNA40981 1490 TCTGGGAATCATTATCTGCCATCAGGCCTGGCTCTTTCCAGGGTTTGATGCACCTTCAA

AC080100 21925 TCTGGGAATCATTATCTGCCATCAGGCCTGGCTCTTTCCAGGGTTTGATGCACCTTCAA
DNA40981 1550 AAACGTGTGGATGATACAGTCCCAGATTCAAGTGATTGAACGGAATGCCTTTGACAACCTT

AC080100 21865 AAACGTGTGGATGATACAGTCCCAGATTCAAGTGATTGAACGGAATGCCTTTGACAACCTT
DNA40981 1610 CAGTCACTAGTGGAGATCAACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTC

AC080100 21805 CAGTCACTAGTGGAGATCAACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTC
DNA40981 1670 TTCACTCCCTTGTCATCATCTAGAGCGGATACATTTACATCACAACCTTGGAACCTGTAAC

AC080100 21745 TTCACTCCCTTGTCATCATCTAGAGCGGATACATTTACATCACAACCTTGGAACCTGTAAC
DNA40981 1730 TGTGACATACTGTGGCTCAGCTGGTGGATAAAAAGACATGGCCCCCTCGAACACAGCTTGT

AC080100 21685 TGTGACATACTGTGGCTCAGCTGGTGGATAAAAAGACATGGCCCCCTCGAACACAGCTTGT
DNA40981 1790 TGTGCCCCGTGTAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAG

AC080100 21625 TGTGCCCCGTGTAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAG
DNA40981 1850 AATTACTTCACATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACT

AC080100 21565 AATTACTTCACATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACT
DNA40981 1910 GAAGGCATGGCAGCTGAGCTGAAATGTCTGGGCTCCACATCCCTGACATCTGTATCTTGG

AC080100 21505 GAAGGCATGGCAGCTGAGCTGAAATGTCTGGGCTCCACATCCCTGACATCTGTATCTTGG

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BLAST RESULTS A-29

DNA40981	1970	ATTACTCCAAATGGAACAGTCATGACACATGGGGCGTACAAAGTGCGGATAGCTGTGCTC
AC080100	21445	ATTACTCCAAATGGAACAGTCATGACACATGGGGCGTACAAAGTGCGGATAGCTGTGCTC
DNA40981	2030	AGTGATGGTACGTAAATTTACAAATGTAAGTGTGCAAGATACAGGCATGTACACATGT
AC080100	21385	AGTGATGGTACGTAAATTTACAAATGTAAGTGTGCAAGATACAGGCATGTACACATGT
DNA40981	2090	ATGGTGAGTAATTCCGTTGGGAATACTACTGCTTCAGCCACCCTGAATGTTACTGCAGCA
AC080100	21325	ATGGTGAGTAATTCCGTTGGGAATACTACTGCTTCAGCCACCCTGAATGTTACTGCAGCA
DNA40981	2150	ACCACTACTCCTTTCTCTTACTTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAG
AC080100	21265	ACCACTACTCCTTTCTCTTACTTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAG
DNA40981	2210	GATGAGGCACGGACCACAGATAACAATGTGGGTCCCCTCCAGTGGTTCGACTGGGAGACC
AC080100	21205	GATGAGGCACGGACCACAGATAACAATGTGGGTCCCCTCCAGTGGTTCGACTGGGAGACC
DNA40981	2270	ACCAATGTGACCACCTCTCTCACACCACAGAGCACAAGGTCGACAGAGAAAACCTTCACC
AC080100	21145	ACCAATGTGACCACCTCTCTCACACCACAGAGCACAAGGTCGACAGAGAAAACCTTCACC
DNA40981	2330	ATCCCAGTGACTGATATAAACAGTGGGATCCCAGGAATTGATGAGGTCATGAAGACTACC
AC080100	21085	ATCCCAGTGACTGATATAAACAGTGGGATCCCAGGAATTGATGAGGTCATGAAGACTACC
DNA40981	2390	AAAATCATCAT'TGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCATT
AC080100	21025	AAAATCATCAT'TGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCATT
DNA40981	2450	TTCTACAAGATGAGGAAGCAGCACCATCGGCAAAACCATCACGCCCCAACAAAGGACTGTT
AC080100	20965	TTCTACAAGATGAGGAAGCAGCACCATCGGCAAAACCATCACGCCCCAACAAAGGACTGTT
DNA40981	2510	GAAATTATTAATGTGGATGATGAGATTACGGGAGACACACCCATGGAAAGCCACCTGCCC
AC080100	20905	GAAATTATTAATGTGGATGATGAGATTACGGGAGACACACCCATGGAAAGCCACCTGCCC
DNA40981	2570	ATGCCTGCTATCGAGCATGAGCACCTAAATCACTATAAATCATACAAATCTCCCTTCAAC
AC080100	20845	ATGCCTGCTATCGAGCATGAGCACCTAAATCACTATAAATCATACAAATCTCCCTTCAAC
DNA40981	2630	CACACAACAACAGTTAACACAATAAATTCATACACAGTTCAGTGCATGAACCGTTATTG
AC080100	20785	CACACAACAACAGTTAACACAATAAATTCATACACAGTTCAGTGCATGAACCGTTATTG
DNA40981	2690	ATCCGAATGAACTCTAAAGACAATGTACAAGAGACTCAAATCTAAAACATTTACAGAGTT
AC080100	20725	ATCCGAATGAACTCTAAAGACAATGTACAAGAGACTCAAATCTAAAACATTTACAGAGTT
DNA40981	2750	ACAAAAAACAAACAATCAAAAAAAGACAGTTTATTAAAAATGACACAAATGACTGGGC
AC080100	20665	ACAAAAAACAAACAATCAAAAAAAGACAGTTTATTAAAAATGACACAAATGACTGGGC
DNA40981	2810	TAAATCTACTGTTTCAAAAAAGTGCTTTACAAAAAACAAAAAGAAAAGAAATTTATT
AC080100	20605	TAAATCTACTGTTTCAAAAAAGTGCTTTACAAAAAACAAAAAGAAAAGAAATTTATT
DNA40981	2870	TATTAAAAATTTCTATTGTGATCTAAAGCAGACAAAA
AC080100	20545	TATTAAAAATTTCTATTGTGATCTAAAGCAGACAAAA

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BLAST RESULTS A-30

(B)

Tue Jul 17 13:25:41 2001 [BLASTP 2.1.3 [Apr-1-2001], NCBI]
/home/ruby/va/Molbio/carpanda/temp1/p1.DNA40981 (640 aa)

Sequences producing High-scoring Segment Pairs:				Score	Match	Pct	E-val
1	P_AAB53089	Human angiogenesis-associated protein PRO3		3362	640	100	0.0
2	P_AAB65292	Human PRO331 protein sequence SEQ ID NO:50		3362	640	100	0.0
3	P_AAB80262	Human PRO331 protein - Homo sapiens.		3362	640	100	0.0
4	P_AAY70673	Human PRO331 protein - Homo sapiens.		3362	640	100	0.0
5	P_AAB24407	Human PRO331 protein sequence SEQ ID NO:10		3362	640	100	0.0
6	P_AAY13394	protein PRO331 - Homo sapiens.		3362	640	100	0.0
7	P_AAW85722	Novel protein (Clone AS209_1) - Homo sapie		3362	640	100	0.0
8	P_AAY08100	Human PRO331 protein - Homo sapiens.		3362	640	100	0.0
9	BAB13406.1	KIAA1580 protein - Homo sapiens		3362	640	100	0.0

>1 P_AAB53089 Human angiogenesis-associated protein PRO331, SEQ ID NO:137 - Homo sapiens. (640 aa) [1 seg]

Score = 3362 (1299 bits), Expect = 0.0

Identities = 640/640 (100%), Positives = 640/640 (100%), at 1,1-640,640

DNA40981	1	MLNKMTLHPQQIMIGPRFNALFDPLLVLALLQLLVVAGLVRAQTCPSCVCSNQFSKV
P_AAB53089	1	MLNKMTLHPQQIMIGPRFNALFDPLLVLALLQLLVVAGLVRAQTCPSCVCSNQFSKV
DNA40981	61	ICVRKNLREVPDGI STNTRLLNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAF
P_AAB53089	61	ICVRKNLREVPDGI STNTRLLNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAF
DNA40981	121	NGLANLNTLELFDNRLTTIPNGAFVYLSKLELWLRNNPIESIPSYAFNRIPSLRRDLG
P_AAB53089	121	NGLANLNTLELFDNRLTTIPNGAFVYLSKLELWLRNNPIESIPSYAFNRIPSLRRDLG
DNA40981	181	ELKRLSYISEGAFEGLSNRLRYNLAMCNLREIPNLTPLIKDELDSLGNHLSAIRPGSFQ
P_AAB53089	181	ELKRLSYISEGAFEGLSNRLRYNLAMCNLREIPNLTPLIKDELDSLGNHLSAIRPGSFQ
DNA40981	241	GLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLH
P_AAB53089	241	GLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLH
DNA40981	301	NPWNCNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPP
P_AAB53089	301	NPWNCNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPP
DNA40981	361	ADLNVTEGMAAELKCRASLSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTQD
P_AAB53089	361	ADLNVTEGMAAELKCRASLSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTQD
DNA40981	421	TGMYTCMVSNSVGNTTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTDNNVGPTP
P_AAB53089	421	TGMYTCMVSNSVGNTTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTDNNVGPTP
DNA40981	481	VVDWETTNVTTSLTPQSTRSTEKFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMA
P_AAB53089	481	VVDWETTNVTTSLTPQSTRSTEKFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMA
DNA40981	541	AVMLVIFYKMRKQHHRQNHHAPTRTVEIINVDDDEITGDTPMESHLMPAIEHEHLNHYS

BLAST RESULTS 8-1

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*****
P_AAB53089 541 AVMLVIFYKMRKQHHRQNHAPTRTVEIINVDDDEITGDTPMESHLMPAIEHEHLNHYS
DNA40981 601 YKSPFNHTTTVTNTINSIHSSVHEPLLIRMNSKDNVQETQI
*****
P_AAB53089 601 YKSPFNHTTTVTNTINSIHSSVHEPLLIRMNSKDNVQETQI

>2 P_AAB65292 Human PRO331 protein sequence SEQ ID NO:501 - Homo sapiens. (640
aa) [1 seg]
Score = 3362 (1299 bits), Expect = 0.0
Identities = 640/640 (100%), Positives = 640/640 (100%), at 1,1-640,640

DNA40981 1 MLNKMTLHPQQIMIGPRFNRALFDPLLVLALLQLLVVAGLVRAQTCPVCSCSNQFSKV
*****
P_AAB65292 1 MLNKMTLHPQQIMIGPRFNRALFDPLLVLALLQLLVVAGLVRAQTCPVCSCSNQFSKV

DNA40981 61 ICVRKNLREVPDGI STNTRLLNLHENQIQI IKVNSFKHLRHLEILQLSRNHIRTIEIGAF
*****
P_AAB65292 61 ICVRKNLREVPDGI STNTRLLNLHENQIQI IKVNSFKHLRHLEILQLSRNHIRTIEIGAF

DNA40981 121 NGLANLNTLELFDNRLTTIPNGAFVYLSKLELWLRNNPIESIPSYAFNRIPSLRRLDLG
*****
P_AAB65292 121 NGLANLNTLELFDNRLTTIPNGAFVYLSKLELWLRNNPIESIPSYAFNRIPSLRRLDLG

DNA40981 181 ELKRLSYISEGAFEGLSNRLRYNLAMCNLREIPNLTPLIKLELDLSDGNHLSAIRPGSFQ
*****
P_AAB65292 181 ELKRLSYISEGAFEGLSNRLRYNLAMCNLREIPNLTPLIKLELDLSDGNHLSAIRPGSFQ

DNA40981 241 GLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLH
*****
P_AAB65292 241 GLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLH

DNA40981 301 NPWNCNCDILWLSWWIKDAPSN TACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPP
*****
P_AAB65292 301 NPWNCNCDILWLSWWIKDAPSN TACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPP

DNA40981 361 ADLNVTEGMAAELKCRAS TSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQD
*****
P_AAB65292 361 ADLNVTEGMAAELKCRAS TSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQD

DNA40981 421 TGMVTCMVNSVGN TTA SATLNVTAA TTT PFSYFSTVTVETMEPSQDEARTTDNNVGPTP
*****
P_AAB65292 421 TGMVTCMVNSVGN TTA SATLNVTAA TTT PFSYFSTVTVETMEPSQDEARTTDNNVGPTP

DNA40981 481 VVDWETTNVT TSLTPQSTRSTEKTF TIPVTDINS GIPGIDEVMKTTKIIIGCFVAITLMA
*****
P_AAB65292 481 VVDWETTNVT TSLTPQSTRSTEKTF TIPVTDINS GIPGIDEVMKTTKIIIGCFVAITLMA

DNA40981 541 AVMLVIFYKMRKQHHRQNHAPTRTVEIINVDDDEITGDTPMESHLMPAIEHEHLNHYS
*****
P_AAB65292 541 AVMLVIFYKMRKQHHRQNHAPTRTVEIINVDDDEITGDTPMESHLMPAIEHEHLNHYS

DNA40981 601 YKSPFNHTTTVTNTINSIHSSVHEPLLIRMNSKDNVQETQI
*****
P_AAB65292 601 YKSPFNHTTTVTNTINSIHSSVHEPLLIRMNSKDNVQETQI

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>3 P_AAB80262 Human PRO331 protein - Homo sapiens. (640 aa) [1 seg]

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Score = 3362 (1299 bits), Expect = 0.0
Identities = 640/640 (100%), Positives = 640/640 (100%), at 1,1-640,640

ENA40981 1 MLNKMTLHPQQIMIGPRFNRAFDPLLVLALLQLLVVAGLVRAQTCPSVCSCSNQFSKV

P_AAB80262 1 MLNKMTLHPQQIMIGPRFNRAFDPLLVLALLQLLVVAGLVRAQTCPSVCSCSNQFSKV

DNA40981 61 ICVRKNLREVPDGI STNTRLLNLHENQIQIIKVN SFKHLRHLEILQLSRNHIRTIEIGAF

P_AAB80262 61 ICVRKNLREVPDGI STNTRLLNLHENQIQIIKVN SFKHLRHLEILQLSRNHIRTIEIGAF

DNA40981 121 NGLANLNTLELFDNRLTTIPNGAFVYLSK LKELWLRNNPIESIPSYAFNRIPSLRRLDLG

P_AAB80262 121 NGLANLNTLELFDNRLTTIPNGAFVYLSK LKELWLRNNPIESIPSYAFNRIPSLRRLDLG

DNA40981 181 ELKRLSYISEGAFEGLSNLRYNL LAMCNLREIPNL TPLIKLDELDSLGNHLSAIRPGSFQ

P_AAB80262 181 ELKRLSYISEGAFEGLSNLRYNL LAMCNLREIPNL TPLIKLDELDSLGNHLSAIRPGSFQ

DNA40981 241 GLMHLQKLWMIQSQIQVIERN AFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIH LHH

P_AAB80262 241 GLMHLQKLWMIQSQIQVIERN AFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIH LHH

DNA40981 301 NPWNCNCDILWLSWWIKD MAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPP

P_AAB80262 301 NPWNCNCDILWLSWWIKD MAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPP

DNA40981 361 ADLNVTEGMAAELKCRAS TSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQD

P_AAB80262 361 ADLNVTEGMAAELKCRAS TSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQD

DNA40981 421 TGMVTCMVSNVSGNTTAS ATLNVTAAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTP

P_AAB80262 421 TGMVTCMVSNVSGNTTAS ATLNVTAAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTP

DNA40981 481 VVDWETTNVTTS LTPQSTRSTEKFTTIPVTDINS GIPGIDEVMKTTKIIIGCFVAITLMA

P_AAB80262 481 VVDWETTNVTTS LTPQSTRSTEKFTTIPVTDINS GIPGIDEVMKTTKIIIGCFVAITLMA

DNA40981 541 AVMLVIFYKMRKQHHRQNH HAPTRTVEIINVDDEITGDT PMESHLPM PAIEHEHLNH YNS

P_AAB80262 541 AVMLVIFYKMRKQHHRQNH HAPTRTVEIINVDDEITGDT PMESHLPM PAIEHEHLNH YNS

DNA40981 601 YKSPFNHTTTVNTINSI HSSVHEPLLIRMNSKDNVQETQI

P_AAB80262 601 YKSPFNHTTTVNTINSI HSSVHEPLLIRMNSKDNVQETQI

>4 P_AAY70673 Human PRO331 protein - Homo sapiens. (640 aa) [1 seg]
Score = 3362 (1299 bits), Expect = 0.0
Identities = 640/640 (100%), Positives = 640/640 (100%), at 1,1-640,640

DNA40981 1 MLNKMTLHPQQIMIGPRFNRAFDPLLVLALLQLLVVAGLVRAQTCPSVCSCSNQFSKV

P_AAY70673 1 MLNKMTLHPQQIMIGPRFNRAFDPLLVLALLQLLVVAGLVRAQTCPSVCSCSNQFSKV

DNA40981 61 ICVRKNLREVPDGI STNTRLLNLHENQIQIIKVN SFKHLRHLEILQLSRNHIRTIEIGAF

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BLAST RESULTS P-3

P_AAY70673 61 ICVRKNLREVPDGI STNTRLLNLHENQIQIIKVN SFKHLRHLEILQLSRNHIRTIEIGAF
DNA40981 121 NGLANLNTLELFDNRLTTIPNGAFVYLSK LKELWLRNNPIESIPSYAFNRIPSLRRDLG

P_AAY70673 121 NGLANLNTLELFDNRLTTIPNGAFVYLSK LKELWLRNNPIESIPSYAFNRIPSLRRDLG
DNA40981 181 ELKRLSYISEGAFEGLSNLRYNL LAMCNLREIPNLTP LIKLDEL DLSGNHLSAIRPGSFQ

P_AAY70673 181 ELKRLSYISEGAFEGLSNLRYNL LAMCNLREIPNLTP LIKLDEL DLSGNHLSAIRPGSFQ
DNA40981 241 GLMHLQKLWMIQSQIQVIERN AFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLER IHLHH

P_AAY70673 241 GLMHLQKLWMIQSQIQVIERN AFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLER IHLHH
DNA40981 301 NPWNCNCDILWLSWWIKD MAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPP

P_AAY70673 301 NPWNCNCDILWLSWWIKD MAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPP
DNA40981 361 ADLNVTEGMAAELKCRAS TSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQD

P_AAY70673 361 ADLNVTEGMAAELKCRAS TSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQD
DNA40981 421 TGMVTCMVSN SVGNTTASATLNVT AATTT PFSYFSTVTVETMEPSQDEARTTDNNVGPTP

P_AAY70673 421 TGMVTCMVSN SVGNTTASATLNVT AATTT PFSYFSTVTVETMEPSQDEARTTDNNVGPTP
DNA40981 481 VVDWETTNVT TSLTPQSTRSTEKTF TIPVTDINS GIPGIDEVMKTTKIIIGCFVAITLMA

P_AAY70673 481 VVDWETTNVT TSLTPQSTRSTEKTF TIPVTDINS GIPGIDEVMKTTKIIIGCFVAITLMA
DNA40981 541 AVMLVIFYKMRKQHHRQNH HAPTRTVEIINVDDEITGDTPMESHLPMPAIEHEHLNHYN S

P_AAY70673 541 AVMLVIFYKMRKQHHRQNH HAPTRTVEIINVDDEITGDTPMESHLPMPAIEHEHLNHYN S
DNA40981 601 YKSPFNHTTTVNTINSI HSSVHEPLLIRMNSKDNVQETQI

P_AAY70673 601 YKSPFNHTTTVNTINSI HSSVHEPLLIRMNSKDNVQETQI

>5 P_AAB24407 Human PRO331 protein sequence SEQ ID NO:107 - Homo sapiens. (640 aa) [1 seg]
Score = 3362 (1299 bits), Expect = 0.0
Identities = 640/640 (100%), Positives = 640/640 (100%), at 1,1-640,640

DNA40981 1 MLNKMTLHPQQIMIGPRFN RALFDPLLVL LALQLLVVAGLVRAQTCPSVCSCSNQFSKV

P_AAB24407 1 MLNKMTLHPQQIMIGPRFN RALFDPLLVL LALQLLVVAGLVRAQTCPSVCSCSNQFSKV
DNA40981 61 ICVRKNLREVPDGI STNTRLLNLHENQIQIIKVN SFKHLRHLEILQLSRNHIRTIEIGAF

P_AAB24407 61 ICVRKNLREVPDGI STNTRLLNLHENQIQIIKVN SFKHLRHLEILQLSRNHIRTIEIGAF
DNA40981 121 NGLANLNTLELFDNRLTTIPNGAFVYLSK LKELWLRNNPIESIPSYAFNRIPSLRRDLG

P_AAB24407 121 NGLANLNTLELFDNRLTTIPNGAFVYLSK LKELWLRNNPIESIPSYAFNRIPSLRRDLG
DNA40981 181 ELKRLSYISEGAFEGLSNLRYNL LAMCNLREIPNLTP LIKLDEL DLSGNHLSAIRPGSFQ

BLAST RESULTS B-4

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APR 17 2002

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BLAST RESULTS 8-9

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P_AAB24407 181 ELKRLSYISEGAFEGLSNLRYNLAMCNLREIPNLTPLIKDELDELDSGNHLSAIRPGSFQ
DNA40981 241 GLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHH
*****
P_AAB24407 241 GLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHH
DNA40981 301 NPWNCNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPP
*****
P_AAB24407 301 NPWNCNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPP
DNA40981 361 ADLNVTEGMAAELKCRASSTLSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQD
*****
P_AAB24407 361 ADLNVTEGMAAELKCRASSTLSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQD
DNA40981 421 TGMVTCMVSNVSGNTTASATLNVTAAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTP
*****
P_AAB24407 421 TGMVTCMVSNVSGNTTASATLNVTAAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTP
DNA40981 481 VVDWETTNVTTSLTQPQSTRSTEKFTTIPVTDINSIGIPGIDEVMKTTKIIIGCFVAITLMA
*****
P_AAB24407 481 VVDWETTNVTTSLTQPQSTRSTEKFTTIPVTDINSIGIPGIDEVMKTTKIIIGCFVAITLMA
DNA40981 541 AVMLVIFYKMRKQHHRQNHHPTRTVEIINVDDDEITGDTPMESHLPMPIAEHEHLNHYS
*****
P_AAB24407 541 AVMLVIFYKMRKQHHRQNHHPTRTVEIINVDDDEITGDTPMESHLPMPIAEHEHLNHYS
DNA40981 601 YKSPFNHTTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI
*****
P_AAB24407 601 YKSPFNHTTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI

>6 P_AAY13394 protein PRO331 - Homo sapiens. (640 aa) [1 seg]
Score = 3362 (1299 bits), Expect = 0.0
Identities = 640/640 (100%), Positives = 640/640 (100%), at 1,1-640,640

DNA40981 1 MLNKMTLHPQQIMIGPRFNRAFDPLLVLALLQLLVVAGLVRAQTCPVSCSCSNQFSKV
*****
P_AAY13394 1 MLNKMTLHPQQIMIGPRFNRAFDPLLVLALLQLLVVAGLVRAQTCPVSCSCSNQFSKV
DNA40981 61 ICVRKNLREVPDGI STNRLNLHENQIQI IKVNSFKHLRHLEILQLSRNHIRTIEIGAF
*****
P_AAY13394 61 ICVRKNLREVPDGI STNRLNLHENQIQI IKVNSFKHLRHLEILQLSRNHIRTIEIGAF
DNA40981 121 NGLANLNTLELFDNRLTTIPNGAFVYLSKLELWLRNNPIESIPSYAFNRIPSLRRLDLG
*****
P_AAY13394 121 NGLANLNTLELFDNRLTTIPNGAFVYLSKLELWLRNNPIESIPSYAFNRIPSLRRLDLG
DNA40981 181 ELKRLSYISEGAFEGLSNLRYNLAMCNLREIPNLTPLIKDELDELDSGNHLSAIRPGSFQ
*****
P_AAY13394 181 ELKRLSYISEGAFEGLSNLRYNLAMCNLREIPNLTPLIKDELDELDSGNHLSAIRPGSFQ
DNA40981 241 GLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHH
*****
P_AAY13394 241 GLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHH
DNA40981 301 NPWNCNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPP
*****
P_AAY13394 301 NPWNCNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPP
```

DNA40981 361 ADLNVTEGMAAELKCRASSTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVD

 P_AAY13394 361 ADLNVTEGMAAELKCRASSTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVD
 DNA40981 421 TGMVTCMVNSVGNNTASATLNVTAAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTP

 P_AAY13394 421 TGMVTCMVNSVGNNTASATLNVTAAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTP
 DNA40981 481 VVDWETTNVTSLTPQSTRSTEKFTTIPVTDINSIGIPGIDEVMKTKIIIGCFVAITLMA

 P_AAY13394 481 VVDWETTNVTSLTPQSTRSTEKFTTIPVTDINSIGIPGIDEVMKTKIIIGCFVAITLMA
 DNA40981 541 AVMLVIFYKMRKQHRRQNHAPTRTVEIINVDDDEITGDTPMESHLPMPAIEHEHLNHYS

 P_AAY13394 541 AVMLVIFYKMRKQHRRQNHAPTRTVEIINVDDDEITGDTPMESHLPMPAIEHEHLNHYS
 DNA40981 601 YKSPFNHTTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI

 P_AAY13394 601 YKSPFNHTTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI

>7 P_AAW85722 Novel protein (Clone AS209_1) - Homo sapiens. (640 aa) [1 seg]
 Score = 3362 (1299 bits), Expect = 0.0
 Identities = 640/640 (100%), Positives = 640/640 (100%), at 1,1-640,640

DNA40981 1 MLNKMTLHPQQIMIGPRFNALFDPLLVLALLQLLVVAGLVRAQTCPVSCSCSNQFSKV

 P_AAW85722 1 MLNKMTLHPQQIMIGPRFNALFDPLLVLALLQLLVVAGLVRAQTCPVSCSCSNQFSKV
 DNA40981 61 ICVRKNLREVPDGI STNTRLNLHENQIQIIKVN SFKHLRHLEILQLSRNHIRTIEIGAF

 P_AAW85722 61 ICVRKNLREVPDGI STNTRLNLHENQIQIIKVN SFKHLRHLEILQLSRNHIRTIEIGAF
 DNA40981 121 NGLANLNTLELFDNRLTTIPNGAFVYLSKLELWLRNNPIESIPSYAFNRIPSLRRDLG

 P_AAW85722 121 NGLANLNTLELFDNRLTTIPNGAFVYLSKLELWLRNNPIESIPSYAFNRIPSLRRDLG
 DNA40981 181 ELKRLSYISEGAFEGLSNRLYNLAMCNLREIPNLTPLIKDELDELDSGNHLSAIRPGSFQ

 P_AAW85722 181 ELKRLSYISEGAFEGLSNRLYNLAMCNLREIPNLTPLIKDELDELDSGNHLSAIRPGSFQ
 DNA40981 241 GLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLH

 P_AAW85722 241 GLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLH
 DNA40981 301 NPWNCNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPP

 P_AAW85722 301 NPWNCNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPP
 DNA40981 361 ADLNVTEGMAAELKCRASSTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVD

 P_AAW85722 361 ADLNVTEGMAAELKCRASSTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVD
 DNA40981 421 TGMVTCMVNSVGNNTASATLNVTAAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTP

 P_AAW85722 421 TGMVTCMVNSVGNNTASATLNVTAAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTP

BLAST RESULTS B-6

DNA40981 481 VVDWETTNVTTS LTPQSTRSTEKFTTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMA

 P_AAW85722 481 VVDWETTNVTTS LTPQSTRSTEKFTTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMA

 DNA40981 541 AVMLVIFYKMRKQHHRQNH HAPTRTVEI INV DDEITGDT PMESHLPMPAIEHEHLNHYS

 P_AAW85722 541 AVMLVIFYKMRKQHHRQNH HAPTRTVEI INV DDEITGDT PMESHLPMPAIEHEHLNHYS

 DNA40981 601 YKSPFNHTTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI

 P_AAW85722 601 YKSPFNHTTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI

 >8 P_AAY08100 Human PRO331 protein - Homo sapiens. (640 aa) [1 seg]
 Score = 3362 (1299 bits), Expect = 0.0
 Identities = 640/640 (100%), Positives = 640/640 (100%), at 1,1-640,640

 DNA40981 1 MLNKMTLHPQQIMIGPRFN RALFDPLL VVLLALQLLVVAGLVRAQTCP SVCS CSNQFSKV

 P_AAY08100 1 MLNKMTLHPQQIMIGPRFN RALFDPLL VVLLALQLLVVAGLVRAQTCP SVCS CSNQFSKV

 DNA40981 61 ICVRKNLREVPD GISTNTRL LN LHENQIQI I K VNSFKHLRHLEILQLSRNHIRTIEIGAF

 P_AAY08100 61 ICVRKNLREVPD GISTNTRL LN LHENQIQI I K VNSFKHLRHLEILQLSRNHIRTIEIGAF

 DNA40981 121 NGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRN NPIESIPSYAFNRIPSLRRLDLG

 P_AAY08100 121 NGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRN NPIESIPSYAFNRIPSLRRLDLG

 DNA40981 181 ELKRLSYISEGAFEGLSNLRYLN LAMCNLREIPNL TPLIKLDEL DLSGNHLSAIRPGSFO

 P_AAY08100 181 ELKRLSYISEGAFEGLSNLRYLN LAMCNLREIPNL TPLIKLDEL DLSGNHLSAIRPGSFO

 DNA40981 241 GLMHLQKLWMIQSQIQVIERN AFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIH LHH

 P_AAY08100 241 GLMHLQKLWMIQSQIQVIERN AFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIH LHH

 DNA40981 301 NPWNCNCDILWLSWWIKD MAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPP

 P_AAY08100 301 NPWNCNCDILWLSWWIKD MAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPP

 DNA40981 361 ADLNVTEGMAAELKCRAS TSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVD

 P_AAY08100 361 ADLNVTEGMAAELKCRAS TSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVD

 DNA40981 421 TGM YTCMVSN SVGN TTASATLNVT AATTT PFSYFSTVT VETMEPSQDEARTTDNNVGPTP

 P_AAY08100 421 TGM YTCMVSN SVGN TTASATLNVT AATTT PFSYFSTVT VETMEPSQDEARTTDNNVGPTP

 DNA40981 481 VVDWETTNVTTS LTPQSTRSTEKFTTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMA

 P_AAY08100 481 VVDWETTNVTTS LTPQSTRSTEKFTTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMA

 DNA40981 541 AVMLVIFYKMRKQHHRQNH HAPTRTVEI INV DDEITGDT PMESHLPMPAIEHEHLNHYS

 P_AAY08100 541 AVMLVIFYKMRKQHHRQNH HAPTRTVEI INV DDEITGDT PMESHLPMPAIEHEHLNHYS

 DNA40981 601 YKSPFNHTTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI

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*****
P_AAY08100 601 YKSPFNHTTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI

>9 BAB13406.1 KIAA1580 protein - Homo sapiens (640 aa) [1 seg]
Score = 3362 (1299 bits), Expect = 0.0
Identities = 640/640 (100%), Positives = 640/640 (100%), at 1,1-640,640

DNA40981 1 MLNKMTLHPQQIMIGPRFNALFDPLLVLALLQLLVVAGLVRAQTCPVSCSCSNQFSKV
*****
BAB13406.1 1 MLNKMTLHPQQIMIGPRFNALFDPLLVLALLQLLVVAGLVRAQTCPVSCSCSNQFSKV

DNA40981 61 ICVRKNLREVPDGI STNTRLLNLHENQIQIIKVN SFKHLRHLEILQLSRNHIRTIEIGAF
*****
BAB13406.1 61 ICVRKNLREVPDGI STNTRLLNLHENQIQIIKVN SFKHLRHLEILQLSRNHIRTIEIGAF

DNA40981 121 NGLANLNTLELFDNRLTTIPNGAFVYLSK LKELWLRNNPIESIPSYAFNRIPSLRRLDLG
*****
BAB13406.1 121 NGLANLNTLELFDNRLTTIPNGAFVYLSK LKELWLRNNPIESIPSYAFNRIPSLRRLDLG

DNA40981 181 ELKRLSYISEGAFEGLSNLRYNL LAMCNLREIPNL TPLIKLDEL DLSGNHLSAIRPGSFQ
*****
BAB13406.1 181 ELKRLSYISEGAFEGLSNLRYNL LAMCNLREIPNL TPLIKLDEL DLSGNHLSAIRPGSFQ

DNA40981 241 GLMHLQKLWMIQSQIQVIERN AFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIH LHH
*****
BAB13406.1 241 GLMHLQKLWMIQSQIQVIERN AFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIH LHH

DNA40981 301 NPWNCNCDILWLSWWIKD MAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPP
*****
BAB13406.1 301 NPWNCNCDILWLSWWIKD MAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPP

DNA40981 361 ADLNVTEGMAAELKCRAS TSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQD
*****
BAB13406.1 361 ADLNVTEGMAAELKCRAS TSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQD

DNA40981 421 TGMVTCMVSN SVGN TTASATLNVTAATTT PFSYFSTVTVETMEPSQDEARTTDNNVGPTP
*****
BAB13406.1 421 TGMVTCMVSN SVGN TTASATLNVTAATTT PFSYFSTVTVETMEPSQDEARTTDNNVGPTP

DNA40981 481 VVDWETTNVT TSLTPQSTRSTEKTF TTPVTDINS GIPGIDEVMKTTKIIIGCFVAITLMA
*****
BAB13406.1 481 VVDWETTNVT TSLTPQSTRSTEKTF TTPVTDINS GIPGIDEVMKTTKIIIGCFVAITLMA

DNA40981 541 AVMLVIFYKMRKQHHRQNH HAPTRTVEIINV DDEITGDTPMESHLPMPAIEHEHLNHYS
*****
BAB13406.1 541 AVMLVIFYKMRKQHHRQNH HAPTRTVEIINV DDEITGDTPMESHLPMPAIEHEHLNHYS

DNA40981 601 YKSPFNHTTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI
*****
BAB13406.1 601 YKSPFNHTTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI

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